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(54) Title: METHOD OF TESTING A MAMMAL FOR ITS PREDISPOSITION FOR FAT CONTENT OF MILK AND/OR ITS PREDISPOSITION FOR MEAT MARBLING

(57) Abstract: The present invention relates to a newly identified nucleic acid sequence of an allele of the polymorphic bovine *DGAT* gene. Moreover, the present invention relates to a method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling.

Method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling

The present invention relates to a newly identified nucleic acid sequence of an allele of the polymorphic bovine *DGAT* gene. Moreover, the present invention relates to a method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling.

Several documents are cited throughout the text of this specification. The disclosure content of the documents cited herein (including any manufacture's specifications, instructions, etc.) is herewith incorporated by reference.

Milk fat content is a continuously distributed trait with heritability estimates between 0.45 and 0.50 (Goddard and Wiggans, 1999). There are considerable differences in the average milk fat content between different cattle breeds, ranging from 3.6% in the Holstein to 4.6% in the Jersey breed. The systematic mapping of quantitative trait loci (QTL) underlying the genetic variance of milk production traits resulted in approximate map positions of QTL for milk fat content (Georges *et al.*, 1995; Zhang *et al.*, 1998; Heyen *et al.*, 1999; Velmala *et al.*, 1999). The most consistent results were reported for a QTL on chromosome 14 (Coppieters *et al.*, 1998) (Riquet *et al.*, 1999). The mapping interval of this QTL could be reduced to a few Centimorgans. High-resolution comparative maps of the critical region did not real obvious positional candidate genes (Riquet *et al.*, 1999). *DGAT*, the gene encoding acyl CoA:diacylglycerol transferase, a microsomal enzyme that catalyses the final step of triglyceride synthesis, became a functional candidate after it had been shown that mice lacking both copies of *DGAT* show defective lactation. This is most likely the consequence of deficient triglyceride synthesis in the mammary gland (Smith *et al.*, 2000).

Another candidate was reported by Barendse et al. (1999). They described a polymorphism in the 5' untranslated region of the gene encoding thyroglobulin (*TG*) which was postulated to be associated with lipid metabolism, particularly the

deposition of fat in muscular tissue. Said deposition of fat produces the typical marbling of the meat. The gene was localized on bovine chromosome 14 very close to the *DGAT* locus (Threadgill et al. 1990). However, the protein encoded by the gene *TG* is not involved in triglyceride synthesis and thus fat deposition.
In summary, the state of the art did so far not provide any genetic link with fat content in milk that can be efficently used in routine testing.

Thus and in of the above, the technical problem underlying the present invention was to provide a method of testing mammals for their predisposition for fat content of milk and/or its predisposition for meat marbling. Said method ought to be easy to use and offer the opportunity to conveniently analyze large nunbers of samples. The solution to this technical problem is achieved by providing the embodiments characterized in the claims.

Accordingly the present invention relates to a nucleic acid molecule encoding a bovine acyl CoA:diacylglycerol transferase (*DGAT*) contributing to or indicative for low fat content of milk and to low meat marbling (intramuscular fat content); wherein said nucleic acid molecule is selected from the group consisting of:

(a) a nucleic acid molecule having or comprising the nucleic acid sequence of SEQ ID NO: 1;
(b) a nucleic acid molecule comprising the coding sequence of the polypeptide of SEQ ID NO: 2;
(c) a nucleic acid molecule the complementary strand of which hybridizes under stringent conditions to the nucleic acid molecule of (a) or (b), wherein said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 1) a guanine and a cytosine residue; and
(d) a nucleic acid molecule the complementary strand of which hybridizes under stringent conditions to the nucleic acid molecule of (a) or (b), wherein said nucleic acid molecule has at the *DGAT* gene (SEQ ID NO: 1) position
    (i) 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine;

(ii) 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine, and 11093 a thymine; or

(iii) 3343 a guanine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine and 11093 a thymine.

Genetic screening (also called genotyping or molecular screening), can be broadly defined as testing to determine if an individual has mutations (alleles or polymorphisms) that either cause a specific phenotype or are "linked" to the mutation causing the phenotype. Linkage refers to the phenomenon that the DNA sequences which are close together in the genome have a tendency to be inherited together. Two or more sequences may be linked because of some selective advantage of co-inheritance. More typically, however, two or more polymorphic sequences are co-inherited because of the relative infrequency with which meiotic recombination events occur within the region between the two polymorphisms. The co-inherited polymorphic alleles are said to be in linkage disequilibrium with one another because, in a given population, they tend to either both occur together or else not occur at all in any particular member of the population. Indeed, where multiple polymorphisms in a given chromosomal region are found to be in linkage disequilibrium with one another, they define a quasi-stable genetic "haplotype." Furthermore, where a phenotype-causing mutation is found within or in linkage with this haplotype, one or more polymorphic alleles of the haplotype can be used as a diagnostic or prognostic indicator of the likelihood of developing a specific phenotype. Identification of a haplotype which spans or is linked to a phenotype-causing mutational change, serves as a predictive measure of an individual's likelihood of having inherited that phenotype-causing mutation. Importantly, such prognostic or diagnostic procedures can be utilized without necessitating the identification and isolation of the actual phenotype-causing molecule. This is significant because the precise determination of the molecular basis of the establishment of a specific phenotype can be difficult and laborious, especially in the case of multifactorial phenotype.

Mapping studies on human chromosome 8 placed *DGAT* indirectly within the mapping interval of the QTL on bovine chromosome 14, the homologous

counterpart of human chromosome 8. Sequencing of *DGAT* from pooled DNA revealed massive frequency shifts at several variable positions between groups of animals with high and low milk fat percentage, respectively. The procedure of said sequencing is described in example 6. It was searched for variation in 10528 basepairs, i.e., the entire coding region of *DGAT*, the major part of the introns and the 5' and 3' regions. 20 variable positions were identified, mostly single nucleotide polymorphisms (summerized in table 9). By said method several nucleotide polymorphisms were detected which were unexpected vis-á-vis the prior art data for the sequences known from the region the *DGAT* in mice, human or plants. Among the variants is a double substitution causing the non-conservative substitution of alanine by lysine. Furthermore, said variants comprised several single nucleotide substitutions. An example for a sequence containing said newly identified polymorphisms is SEQ ID NO: 1.

Direct sequencing in animals belonging to different breeds of Bos taurus taurus and Bos taurus indicus as well as in animals of *Bos grunniens* (yak) and *Bubalus bubalus* (water buffalo) at position 3343, 10433, 10434, 11030, 11048 and 11093 allowed to derive at least 8 haplotypes (see Fig. 12). The haplotypes observed encoded a DGAT1 protein with either a lysine or an alanine in position 232 of the DGAT1 polypeptide sequence. In addition, specific nucleotides at positions 3343, 10433, 10434, 11030, 11048 and 11093 were demonstrated to be indicative of a specific haplotype. As shown in Fig. 12A, haplotypes encoding a protein with a lysine in position 232 may contain in the above mentioned positions either TAAGCC, CAAGCC, CAAGCT, CAAACC or CAAACT while alanine encoding haplotypes are characterized by CGCGCT (i.e. at position: 3343 cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine), CGCGTT (i.e. at position: 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine, and 11093 a thymine) or GGCGTT (i.e. at position: 3343 a guanine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine and 11093 a thymine) in the above mentioned positions. It is of note that the invention also comprises sequences wherein one or two nucleotides in the above-indicated positions are exchanged by different nucleotides. In addition, the invention comprises haplotypes arising from recombination events and including the above recited gene.

Furthermore, an RFLP analysis revealed frequency estimates for lysine and alanine encoding alleles in several cattle breeds of Bovinae subfamilies (see Fig. 12b). Distinct frequency differences for the allelic distribution in various breeds indicated a correlation between milk fat content and the genetic variation.

The term "hybridizes under stringent conditions", as used in the description of the present invention, is well known to the skilled artisian and corresponds to conditions of high stringency. Appropriate stringent hybridization conditions for each sequence may be established by a person skilled in the art on well-known parameters such as temperature, composition of the nucleic acid molecules, salt conditions etc.; see, for example, Sambrook et al., "Molecular Cloning, A Laboratory Manual"; CSH Press, Cold Spring Harbor, 1989 or Higgins and Hames (eds.), "Nucleic acid hybridization, a practical approach", IRL Press, Oxford 1985, see in particular the chapter "Hybridization Strategy" by Britten & Davidson, 3 to 15. Stringent hybridization conditions are, for example, conditions comprising overnight incubation at 42° C in a solution comprising: 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°. Other stringent hybridization conditions are for example 0.2 x SSC (0.03 M NaCl, 0.003M Natriumcitrat, pH 7) bei 65°C. Preferred in accordance with the present invention are nucleic acids which are capable of hybridizing to the nucleic acid molecule of the invention or parts thereof wherein said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 1) a guanine and a cytosine residue. More preferred in accordance with the present invention are nucleic acids which are capable of hybridizing to the complementary strand of any of the nucleic acid molecules of the invention or parts thereof, wherein said nucleic acid molecule contains at position 3343, 10433, 10434, 11030, 11048 and 11093 of the *DGAT* gene (SEQ ID NO: 1) nucleotides which are either CGCGCT, CGCGTT or GGCGTT. Furthermore, the nucleic acid molecules of the invention may contain any alanine codon at the position encoding amino acid 232 of DGAT.

The term "corresponding" as used herein means that a position is not only determined by the number of the preceding nucleotides and amino acids,

respectively. The position of a given nucleotide or amino acid in accordance with the present invention which may be deleted, substituted or comprise one or more additional nucleotide(s) may vary due to deletions or additional nucleotides or amino acids elsewhere in the gene or the polypeptide. Thus, under a "corresponding position" in accordance with the present invention it is to be understood that nucleotides or amino acids may differ in the indicated number but may still have similar neighboring nucleotides or amino acids. Said nucleotides or amino acids may for instance together with their neighbors form sequences which may be involved in the regulation of gene expression, stability of the corresponding RNA or RNA editing, as well as encode functional domains or motifs of the protein of the invention. In the context of the invention functional domains or motifs of the invention are defined as portions having the enzymatic activity of *DGAT* and/or portions which are capable to be recognized as an antigen and therefore represent an epitope for an antibody or small molecule.

Therefore, the invention comprises allelic variants of the *DGAT* gene as well as recombinantly or otherwise altered *DGAT* sequences. In conformance with the present invention, the recited nucleic acid "encodes" the *DGAT* enzyme. Whereas by definition the claimed nucleic acid molecule comprises the coding region, it may also comprise non-coding regions such as regulatory reigns or introns.

Apart from being the subject of investigation, the nucleic acid molecule of the invention may be useful as probes in Northern or Southern Blot analysis of RNA or DNA preparations, respectively, or can be used as oligonucleotide primers in PCR analysis dependent on their respective size. Also comprised by the invention are hybridizing nucleic acids which are useful for analyzing DNA-Protein interactions via, e.g., electrophoretic mobility shift analysis (EMSA). Preferably, said hybridizing nucleic acids comprise at least 10, more preferably at least 15 nucleotides in length while a hybridizing polynucleotide of the present invention to be used as a probe preferably comprises at least 100, more preferably at least 200, or most preferably at least 500 nucleotides in length.

The nucleic acid molecule of the invention is expected to occur in any breed of the bovine species. In a preferred embodiment of the invention the bovine nucleic acid molecule is a nucleic acid molecule of a bovine animal selected from the group

consisting of Ayrshire, Bazadaise, Beefalo, Blaarkop, Braunvieh Fleischnutzung, Grauvieh, Lakenfelder, Limpurger Fleischnutzung, Maine Anjou, Marchigiana, Montbeliard, Murnau-Werdenfelser, Normanne, Romagnola, Rotbunt Fleischnutzung, Telemark, Tuxer, Vogesen-Rind, Wasserbüffel, Witrug, Yak, Auerochse, Bison/Wisent, Hinterwälder Fleischnutzung, Vorderwälder Fleischnutzung, Angler, Doppelnutzung Rotbunt, Holstein-Rbt., Holstein-Sbt., Holstein-Friesian, Deutsches Shorthorn, Rotvieh alter Angler, Aberdeen Angus, Aubrac, Blonde d'Aqultaine, Brahman, Brangus, Charolais, Chlanina, Deutsche Angus, Fjall-Rind, Fleckvieh Fleischnutzung Ost, Gelbvieh Fleischnutzung, Hereford, Jersey, Limousin, Lincoln Red, Piemonteser, Salers, South Devon, Weißblaue Belgier, Beited Galloway, Dexter, Galloway, Highland, Longhorn, Luing, Ungarisches Steppenrind, Welsh-Black, White Galloway, White Park, Zwerg-Zebus, Rotvieh Zuchtrichtung, Uckermärker, Deutsche Schwarzbunte alter, Braunvieh, Fleckvieh, Gelbvieh, Pinzgauer Fleischnutzung, Ansbach-Triesdorfer, Braunvieh alter Zuchtrichtung, Limpurger, Murnau-Werdenfelser, Pinzgauer, Pustertaler Schecken, Hinterwäldler, Vorderwäldler and Glanrind.

In a more preferred embodiment of the invention the bovine nucleic acid molecule is a nucleic acid molecule of a female bovine animal.

The nucleic acid molecule can be taken from any nucleic acid containing tissue. Preferably said nucleic acid molecule is present in a sample taken from, for example, from muscle, blood, skin, milk, urine and other samples taken from a bovine animal.

Preferably said nucleic acid molecule is mRNA, genomic DNA (gDNA) or cDNA which is derived from said mRNA by reverse transcription of said mRNA.
The method or reverse transcription of mRNA into cDNA is well established and known by a person skilled in the art.

More preferably said gDNA is a gene.

In an preferred embodiment of the invention the nucleic acid molecule is a fragment of the herein above described nucleic acid molecule having at least 14 nucleotides wherein said fragment comprises nucleotide position 10433 and 10434 of SEQ ID NO: 1.

Said nucleic acid molecule may, for example, be used as hybridization probe. For hybridization probes, it may be, e.g., desirable to use nucleic acid analogs, in order to improve the stability and binding affinity. The term "nucleic acid" shall be understood to encompass such analogs. A number of modifications have been described that alter the chemistry of the phosphodiester backbone, sugars or heterocyclic bases. Among useful changes in the backbone chemistry are phosphorothioates; phosphorodithioates, where both of the non-bridging oxygens are substituted with sulfur; phosphoroamidites; alkyl phosphotriesters and boranophosphates. Achiral phosphate derivatives include 3'-O'-5'-S-phosphorothioate, 3'-S-5'-O-phosphorothioate, 3'-CH2-5'-O-phosphonate and 3'-NH-5'-O-phosphoroamidate. Peptide nucleic acids replace the entire phosphodiester backbone with a peptide linkage. Sugar modifications are also used to enhance stability and affinity. The a-anomer of deoxyribose may be used, where the base is inverted with respect to the natural b-anomer. The 2'-OH of the ribose sugar may be altered to form 2'-O-methyl or 2'-O-allyl sugars, which provides resistance to degradation without comprising affinity. Modification of the heterocyclic bases must maintain proper base pairing. Some useful substitutions include deoxyuridine for deoxythymidine; 5-methyl-2'-deoxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. 5-propynyl-2'-deoxyuridine and 5-propynyl-2'-deoxycytidine have been shown to increase affinity and biological activity when substituted for deoxythymidine and deoxycytidine, respectively.

The hybridization probe or the primer(s) used for amplification may also contain a detectable label. Suitable labels include fluorochromes, e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine(ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), radioactive labels, e.g. ^{32}P, ^{35}S, ^{3}H; etc. The label may also be a two stage system, where the DNA is conjugated to biotin, haptens, etc. having a high

affinity binding partner, e.g. avidin, specific antibodies, etc., where the binding partner is conjugated to a detectable label. In the case of amplification the label may be conjugated to one or both of the primers. The pool of nucleotides used in the amplification may also be labeled, so as to incorporate the label into the amplification product. Alternatively, the double strand formed after hybridization can be detected by anti-double strand DNA specific antibodies or aptamers etc.

More preferably said nucleic acid molecule is complementary to the above described nucleic acid. Said complementary nucleic acid molecule is suitable to hybridize specifically with a polynucleotide as described above. Specific hybridization occurs preferably under stringent conditions and implies no or very little cross-hybridization with nucleotide sequences encoding no or substantially different proteins. Such nucleic acid molecules may be used as probes and/or for the control of gene expression. Nucleic acid probe technology is well known to those skilled in the art who will readily appreciate that such probes may vary in length. Preferred are nucleic acid probes of 17 to 35 nucleotides in length. Of course, it may also be appropriate to use nucleic acids of up to 100 and more nucleotides in length. The nucleic acid probes of the invention are useful for various applications. On the one hand, they may be used as PCR primers for amplification of nucleic acid molecules according to the invention. Another application is the use as a hybridization probe to identify polynucleotides hybridizing to the nucleic acid molecule of the invention by homology screening of genomic DNA libraries (see example 3). Nucleic acid molecules according to this preferred embodiment of the invention which are complementary to a polynucleotide as described above may also be used for repression of expression of a gene comprising such a polynucleotide, for example due to an antisense or triple helix effect or for the construction of appropriate ribozymes (see, e.g., EP-A1 0 291 533, EP-A1 0 321 201, EP-A2 0 360 257) which specifically cleave the (pre)-mRNA of a gene comprising a polynucleotide of the invention. Selection of appropriate target sites and corresponding ribozymes can be done as described for example in Steinecke, Ribozymes, Methods in Cell Biology 50, Galbraith et al. eds Academic Press, Inc. (1995), 449-460. Standard methods relating to antisense technology have also been described (Melani, Cancer Res. 51 (1991), 2897-2901). Furthermore, the

person skilled in the art is well aware that it is also possible to label such a nucleic acid probe with an appropriate marker for specific applications, such as for the detection of the presence of a polynucleotide of the invention in a sample derived from an organism.

The above described nucleic acid molecules may either be DNA or RNA or a hybrid thereof. Furthermore, said nucleic acid molecule may contain, for example, thioester bonds and/or nucleotide analogues, commonly used in oligonucleotide anti-sense approaches. Said modifications may be useful for the stabilization of the nucleic acid molecule against endo- and/or exonucleases in the cell. Said nucleic acid molecules may be transcribed by an appropriate vector containing a chimeric gene which allows for the transcription of said nucleic acid molecule in the cell. Such nucleic acid molecules may further contain ribozyme sequences as described above.

Furthermore, the present invention provides a vector comprising the herein above described nucleic acid molecule. Said expression vectors may particularly be plasmids, cosmids, viruses or bacteriophages used conventionally in genetic engineering plasmids, cosmids, viruses and bacteriophages used conventionally in genetic engineering that comprise the aforementioned nucleic acid. Preferably, said vector is a gene transfer or targeting vector. Expression vectors derived from viruses such as retroviruses, vaccinia virus, adeno-associated virus, herpes viruses, or bovine papilloma virus, may be used for delivery of the nucleic acid into targeted cell population. Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors; see, for example, the techniques described in Sambrook et al., Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y. and Ausubel et al., Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. (1989). Alternatively, the nucleic acids and vectors can be reconstituted into liposomes for delivery to target cells. The vectors containing the nucleic acid can be transferred into the host cell by well-known methods, which vary depending on the type of cellular host. For example, calcium phosphate or DEAE-Dextran mediated transfection or electroporation may be used for eukaryotic cellular hosts; see Sambrook, supra. Such vectors may comprise further genes such as marker genes

which allow for the selection of said vector in a suitable host cell and under suitable conditions.

Preferably, said vector comprises regulatory elements for expression of said nucleic acid molecule. Consequently, the nucleic acid of the invention may be operatively linked to expression control sequences allowing expression in eukaryotic cells. Expression of said nucleic acid molecule comprises transcription of the sequence nucleic acid molecule into a translatable mRNA. Regulatory elements ensuring expression in eukaryotic cells, preferably mammalian cells, are well known to those skilled in the art. They usually comprise regulatory sequences ensuring initiation of transcription and, optionally, a poly-A signal ensuring termination of transcription and stabilization of the transcript, and/or an intron further enhancing expression of said nucleic acid. Additional regulatory elements may include transcriptional as well as translational enhancers, and/or naturally-associated or heterologous promoter regions. Possible regulatory elements permitting expression in eukaryotic host cells are the AOX1 or GAL1 promoter in yeast or the CMV-, SV40-, RSV-promoter (Rous sarcoma virus), CMV-enhancer, SV40-enhancer or a globin intron in mammalian and other animal cells. Beside elements which are responsible for the initiation of transcription such regulatory elements may also comprise transcription termination signals, such as the SV40-poly-A site or the tk-poly-A site, downstream of the nucleic acid molecule. Furthermore, depending on the expression system used leader sequences capable of directing the polypeptide to a cellular compartment or secreting it into the medium may be added to the coding sequence of the aforementioned nucleic acid and are well known in the art. The leader sequence(s) is (are) assembled in appropriate phase with translation, initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein, or a portion thereof, into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode .a fusion protein including an C- or N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. In this context, suitable expression vectors are known in the art such as Okayama-Berg cDNA expression vector pcDVI (Pharmacia), pCDM8, pRc/CMV, pcDNA1, pcDNA3,

the Echo™ Cloning System (Invitrogen), pSPORT1 (GIBCO BRL) or pRevTet-On/pRevTet-Off or pCI (Promega).

Another preferred embodiment of the invention relates to primer or primer pair, wherein the primer or primer pair hybridize under stringent conditions to the nucleic acid molecule of the invention comprising nucleotide position 10433 and 10434 of SEQ ID NO: 1 or the complement strand thereof. The exact composition of the primer sequences is not critical as long as they allow detection of the desired sequence(s). Preferably, the primers are chosen in such a way that they hybridize under stringent conditions to the desired sequence(s). It is preferable to choose a primer or a pair of primers that will generate an amplification product of at least 50 nt, preferably of at least about 100 nt and most preferably of at least 200 nt. Algorithms for the selection of primer sequences are generally known and are available in commercial software packages (see example 1). Amplification primers hybridize to complementary strands of DNA and will prime towards each other.

Furthermore, the present invention relates to a host cell which contains the herewith above described expression vector.
Preferably, said host cell is a eukaryotic, most preferably a mammalian cell if therapeutic uses of the protein are envisaged. Of course, yeast and less preferred prokaryotic, e.g., bacterial cells may serve as well, in particular if the produced protein is used as a diagnostic means.
The polynucleotide or vector of the invention which is present in the host cell may either be integrated into the genome of the host cell or it may be maintained extrachromosomally.
The term "prokaryotic" is meant to include all bacteria which can be transformed or transfected with a DNA or RNA molecules for the expression of a protein of the invention. Prokaryotic hosts may include gram negative as well as gram positive bacteria such as, for example, E. coli, S. typhimurium, Serratia marcescens and Bacillus subtilis. The term "eukaryotic" is meant to include yeast, higher plant, insect and preferably mammalian cells. Depending upon the host employed in a recombinant production procedure, the protein encoded by the polynucleotide of the present invention may be glycosylated or may be non-glycosylated. A nucleic acid

molecule of the invention can be used to transform or transfect the host using any of the techniques commonly known to those of ordinary skill in the art. Furthermore, methods for preparing fused, operably linked genes and expressing them in, e.g., mammalian cells and bacteria are well-known in the art (Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). The genetic constructs and methods described therein can be utilized for expression of the protein of SEQ ID NO: 2 in eukaryotic or prokaryotic hosts. In general, expression vectors containing promoter sequences which facilitate the efficient transcription of the inserted polynucleotide are used in connection with the host. The expression vector typically contains an origin of replication, a promoter, and a terminator, as well as specific genes which are capable of providing phenotypic selection of the transformed cells.

In an alternative embodiment the present invention relates to a method for production of a functional bovine *DGAT* or a functional fragment thereof comprising:

(a) culturing said host cell containing the expression vector which comprises the herein above mentioned nucleic acid molecule under conditions allowing the expression of the encoded polypeptide; and

(b) collecting the polypeptide from the culture.

As aforementioned, a functional fragment is defined in the context of the present invention as a fragment having the enzymatic activity of *DGAT* and/or fragment which is capable to be recognized as an antigen and therefore represent an epitope for an antibody and/or small molecule suitable for specific binding and detection of an epitope.

The transformed hosts can be grown in fermentors and cultured according to techniques known in the art to achieve optimal cell growth. The protein of the invention can then be isolated from the growth medium, cellular lysates, or cellular membrane fractions. Once expressed, the protein of the present invention can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, gel electrophoresis and the like; see, Scopes, "Protein Purification", Springer-Verlag, N.Y. (1982). Substantially pure proteins of at least about 90 to 95% homogeneity are preferred, and 98 to 99% or more homogeneity are most preferred, for pharmaceutical uses. Once purified,

partially or to homogeneity as desired, the proteins may then be used therapeutically (including extracorporeally) or in developing and performing assay procedures.

Hence, in a still further embodiment, the present invention relates to functional bovine *DGAT* polypeptide as depicted in SEQ ID NO: 2 or a functional fragment thereof encoded by a nucleic acid molecule (SEQ ID NO: 1) or produced by a method of as described above. It will be apparent to those skilled in the art that the protein of the invention can be further coupled to other moieties for, e.g., drug targeting and imaging applications. Such coupling may be conducted chemically after expression of the protein to site of attachment or the coupling product may be engineered into the protein of the invention at the DNA level. The DNAs are then expressed in a suitable host system, and the expressed proteins are collected and renatured, if necessary.

Furthermore, the provision of the protein of the present invention enables the production of *DGAT* specific antibody which binds to an epitope of the polypeptide or fragment of SEQ ID NO: 2 the epitope comprising a alanine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 4 having a lysine at position 232. In an alternative embodiment the invention relates to the production of *DGAT* specific antibody which binds to an epitope of the polypeptide or fragment of SEQ ID NO: 4 the epitope comprising a lysine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 2 having a alanine at position 232.
In this respect, hybridoma technology enables production of cell lines secreting antibody to essentially any desired substance that produces an immune response. RNA encoding the light and heavy chains of the immunoglobulin can then be obtained from the cytoplasm of the hybridoma. The 5' end portion of the mRNA can be used to prepare cDNA to be inserted into an expression vector. The DNA encoding the antibody or its immunoglobulin chains can subsequently be expressed in cells, preferably mammalian cells.
Depending on the host cell, renaturation techniques may be required to attain proper conformation of the antibody. If necessary, point substitutions seeking to

optimize binding may be made in the DNA using conventional cassette mutagenesis or other protein engineering methodology such as is disclosed herein.

Said antibodies, which are monoclonal antibodies, polyclonal antibodies, single chain antibodies, or fragment thereof that specifically binds said peptide or polypeptide also including bispecific antibody, synthetic antibody, antibody fragment, such as Fab, a $F(ab_2)'$, Fv or scFv fragments etc., or a chemically modified derivative of any of these (all comprised by the term "antibody"). Monoclonal antibodies can be prepared, for example, by the techniques as originally described in Köhler and Milstein, Nature 256 (1975), 495, and Galfré, Meth. Enzymol. 73 (1981), 3, which comprise the fusion of mouse myeloma cells to spleen cells derived from immunized mammals with modifications developed by the art. Furthermore, antibodies or fragments thereof to the aforementioned peptides can be obtained by using methods which are described, e.g., in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. When derivatives of said antibodies are obtained by the phage display technique, surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of the peptide or polypeptide of the invention (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13). The production of chimeric antibodies is described, for example, in WO89/09622. A further source of antibodies to be utilized in accordance with the present invention are so-called xenogenic antibodies. The general principle for the production of xenogenic antibodies such as human antibodies in mice is described in, e.g., WO 91/10741, WO 94/02602, WO 96/34096 and WO 96/33735. Antibodies to be employed in accordance with the invention or their corresponding immunoglobulin chain(s) can be further modified using conventional techniques known in the art, for example, by using amino acid deletion(s), insertion(s), substitution(s), addition(s), and/or recombination(s) and/or any other modification(s) known in the art either alone or in combination. Methods for introducing such modifications in the DNA sequence underlying the amino acid sequence of an immunoglobulin chain are well known to the person skilled in the art; see, e.g., Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y.

Moreover, the present invention relates to a transgenic, non-human animal comprising at least the herein above disclosed nucleic acid molecules. Preferably said transgenic, non-human animal belongs to cattle.

In an other embodiment the present invention relates to a method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling comprising analyzing the nucleic acid of a sample comprising the gene encoding *DGAT*, a corresponding mRNA for nucleotide polymorphisms which are connected with said predisposition or any nucleic acid molecule of the invention. The term "its predisposition for fat content of milk and/or its predisposition for meat marbling" describes the capability of a mammal to produce milk with high fat, respectively low fat content and/or its capability to produce meat with high intramuscular fat content, respectively low intramuscular fat content.

Preferably the nucleic acid of said method is DNA.

More preferably the nucleic acid of said method is gDNA (genomic DNA).

Also more preferred the nucleic acid is cDNA which is derived from said mRNA by reverse transcription of said mRNA.

In accordance with the invention the nucleotide polymorphisms which are contributing to or indicative for low fat content of milk and to low meat marbling are in one preferred embodiment located in the coding region of the *DGAT* gene.

More preferably the nucleotide polymorphisms in the coding region of the gene encoding *DGAT* result in substitution, deletion and/or addition of at least one amino acid in the amino acid sequence of the polypeptide which is encoded by said gene.

Further more preferably said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 1) a guanine and a cytosine residue which corresponds to i.e. correlates with a predisposition for low fat content of milk and low meat marbling.

More preferably the nucleic acid molecule has at the positions corresponding to position 3343, 10433, 10434, 11030, 11048 and 11093 of the DGAT gene (SEQ ID NO:1) the nucleotides CGCGCT (i.e. at position 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine), CGCGTT (i.e. at position 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine, and 11093 a thymine) or GGCGTT (i.e. at position 3343 a guanine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine and 11093 a thymine) which corresponds to i.e. correlates with a predisposition for low fat content of milk and low meat marbling.

Alternatively said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 3) two adenine residue which corresponds to i.e. correlates with a predisposition for high fat content of milk and high meat marbling.

More preferably said nucleic acid molecule has at the positions corresponding to positions 3343, 10433, 10434, 11030, 11048 and 11093 of the DGAT gene the nucleotides TAAGCC (i.e. at position 3343 a thymine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine and 11093 a cytosine), CAAGCC (i.e. at position 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine, and 11093 a cytosine), CAAGCT (i.e. at position 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine), CAAACC (i.e. at position 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 an adenosine, 11048 a cytosine and 11093 a cytosine) or CAAACT (i.e. at position 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 an adenosine, 11048 a cytosine and 11093 a thymine) which corresponds to i.e. correlates with a predisposition for high fat content of milk and high meat marbling.

Also in accordance with the invention the nucleotide polymorphisms are preferably located in a region which is responsible for the regulation of the expression of the product of the gene encoding *DGAT*.

More preferred the nucleotide polymorphisms which are analyzed by the method of the invention are single nucleotide polymorphisms (SNP).

In another preferred embodiment said testing in the method of the invention comprises hybridizing a herein above described nucleic acid molecule as a probe under stringent conditions to the nucleic acid molecules comprised in said sample and detecting hybridization. Such stringent conditions are known by a person skilled in the art and also described herein above.

More preferably said testing comprises digesting the product of said hybridization with a restriction endonuclease and analyzing the product of said digestion.

Even more preferred said probe is detectably labeled.

Alternatively, said testing comprises determining the nucleic acid sequence of at least a portion of said nucleic acid molecule. Methods for sequencing of nucleic acids are known in the art. An example for said testing for predisposition of individual animals by comparative sequencing is described herein below in example 6.

Preferably said determination of the nucleic acid sequence is effected by solid-phase minisequencing.

Also alternatively the testing further comprises, prior to analyzing the nucleic acid, amplification of at least a portion of said nucleic acid.

More preferred in said amplification reaction at least one of the primers employed in said amplification reaction is the primer or belongs to the primer pair as aforementioned, the method comprising assaying for an amplification product.

Even more preferred said amplification is effected by or said amplification is the polymerase chain reaction (PCR).

Furthermore, alternatively the method of the invention further comprises analyzing said nucleic acid by the use of:

(a) a primer extension assay;

(b) a differential hybridization assay; and/or

(c) an assay which detects allele-specific enzyme cleavage.

The underlying principles and the use of said assays has been described in an article of Asil Memisoglu (www.thebiotechclub.org/Tech/pharmacogenomics.html). Examples for said assays are known by a person skilled in the art. Furthermore, the method of analyzing said nucleic acid by the use of an assay which detects allele-specific enzyme cleavage is describe in example 8 herein below.

Furthermore, in an other embodiment the invention relates to a method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling, said method comprising the steps of:

(a) preparation of a tissue sample from the subject;

(b) contacting the sample with an aforementioned antibody specifically binding to an epitope of the polypeptide or fragment of SEQ ID NO: 2 the epitope comprising a alanine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 4 having a lysine at position 232 or specifically binding to an epitope of the polypeptide or fragment of SEQ ID NO: 4 the epitope comprising a lysine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 2 having a alanine at position 232; and

(c) detecting whether a specific binding of said antibody to its antigen has occurred.

Said method may comprise the transfer of the sample onto a membrane, e.g. by blot technique after electrophoresis. If so the detection whether a specific binding has occurred may comprise washing of the membrane to remove agent unspecifically bound to the membrane. Said detection may be performed by the use of agents which on the one hand are suitable for the detection of the presence of the specifically interacting agent. Furthermore said agents may comprises a domain or function which can be used for the generation of a detectable signal. The steps of contacting the proteins with said agents and detecting whether a specific interaction

has occurred may be similar to the principle of immunodetection of proteins by Western Blot known to the person skilled in the art.

Preferably said method wherein the binding of the antibody which specifically binds to an epitope of the polypeptide or fragment of SEQ ID NO: 2 the epitope comprising a alanine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 4 having a lysine at position 232 indicates a predisposition of the mammal for low fat content of milk and to low meat marbling.

Also preferred, said method wherein the binding of the antibody which specifically binds to an epitope of the polypeptide or fragment of SEQ ID NO: 4 the epitope comprising a lysine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 2 having a alanine at position 232 indicates a predisposition of the mammal for high fat content of milk and to high meat marbling.
Also preferred is a method for testing of a mammal for its predisposition for low fat content and/or its predisposition for meat marbling comprising analyzing nucleotide positions 3343, 10433, 10434, 11030, 11048 and 11093 of the DGAT gene (SEQ ID NO:1), wherein the nucleotides CGCGCT, CGCGTT or GGCGTT at the above-indicated positions are indicative of low fat content of milk and low meat marbling.

Also preferred is a method for testing of a mammal for its predisposition for high fat content and/or its predisposition for meat marbling comprising analyzing nucleotide positions 3343, 10433, 10434, 11030, 11048 and 11093 of the DGAT gene (SEQ ID NO:1), wherein the nucleotides TAAGCC, CAAGCC, CAAGCT, CAAACC or CAAACT at the above-indicated positions are indicative of high fat content of milk and high meat marbling.

More preferred the samples which are analyzed by the methods of the invention are isolated from cloven hoofed animals.

In a further more preferred embodiment said cloven hoofed animals are cattle, buffalos, yaks or pigs.

Finally the present invention relates in one embodiment to a kit comprising at least the aforementioned fragment, the aforementioned nucleic acid molecule, the aforementioned primer or primer pair , or one of the aforementioned in one or more containers.

The figures show

Figure 1 Bovine metaphase spread after fluorescence in situ hybridization using BAC clone 56-F1. BAC-DNA was labeled with biotin using nick-translation. Detection of the hybridized probe was performed with streptavidin-Cy3. Photos were taken with a CCD-camera coupled to a Zeiss microscope with a magnification of 650 x. The signals on both copies of chromosome 14 are indicated by arrow and arrow head. Note that one copy of chromosome 14 (signal indicated by arrow) is involved in a Robertsian fusion with chromosome 20.

Figure 2 Partial maps of three BACs (56-F1, 240-A1, 269-H17). Solid lines represent sequenced parts. The vector sequences are shown as gray boxes. T7 and SP6 refer to the primers used for BAC-end sequencing. The colored boxes represent genes: *DGAT*, diacylglycerol acyltransferase; *HSF1*, heat shock transcription factor 1; *FPXL6*, f-box and leucine-rich repeat protein 6. Annotation of the sequences is based on a high similarity with the corresponding human sequences. The arrows indicate the orientation of the genes. Drawings are not to scale.

Figure 3 EST-derived transcript map of the bovine DGAT gene. The blue areas represent sequences covered by the ESTs. T0 is composed of ESTs AW483961, AW486026, AW652329, BE664362, BE753833, BE664357, T1 of AW446908, T2 of AW446985, T4 of AW326076 and T5 of BE486748. The approximate position of stop codons are indicated by asterisks. T1 and T2 may represent alternative transcripts, with T1 leading to a truncated gene product. T3 contains 28 bp that are not found in the genomic sequence and therefore most likely are artefacts. T4 and T5 probably represent unprocessed transcripts.

Figure 4 Bovine genomic sequence containing *DGAT* and parts of *HSF1* (3'end). Start codon (position3605), stop codon (position 11906) and polyA signal (position 12163) of *DGAT* and stop codon (position 13731) and putative polyA signal (position 13439) of *HSF1* are in bold.

Figure 5 Variable PCR amplification by a, individual animals and b, pooled samples.

Figure 6 Consed views of sequencing traces for positions 10430-10437 within *DGAT* demonstrating the effect of DMSO in the PCR at variable positions 14433 and 14434 of a heterozygous animal (GC/ AA). a, three repetitions without DMSO. b, three repetitions with 5% DMSO. Average normalized amplitude values (± standard deviation) in a: A 1.06±0.25, A 0.61±0.16, G 0.56±0.31, C 0.21±0.14; in b: A 0.42±0.02, A 0.22±0.02, G 1.38±0.02 C 0.59±0.03.

Figure 7 Consed views of sequencing traces for positions 10430-10437 within the *DGAT* coding sequence. Positions 10433 and 10434 are variable. (a), (b) represent homozygous animals (GC/GC, AA/ AA), respectively) and (c) a heterozygous animal (AA/GC). (d) and (e) show the frequency shift between the pools FVpool12+ (breeding value milk fat % (BVMF) = +0.729±0.045) and FVpool12- (BVMF = -0.445±0.042), (f) and (g) between pools FVpool32+ (BVMF = +0.669±0.063) andFVpool32- (BVMF = -0.381±0.059), (h) and (i) between pools BVpool20+ (BVMV = +0.421±0.113) and BVpool20- (BVMF = -0.305±0.057).

Figure 8 Allelic frequencies in pooled samples from animals with high (FV12+, FV32+, BV20+) and low (FV12-, FV32-, BV20-) breeding values for milk fat content at variable positions in and around *DGAT*. The numbers below the x-axis refer to the following positions (according to the numbering in Figure 3): 1, 3343; 2, 8567; 3, 8607; 4, 9284; 5, 10433; 6, 10434; 7, 11030; 8, 11048; 9, 11993; 10, 130309. The variable positions 5 and 6 are responsible for the K232A substitution, with the frequency of the A-encoding allele being indicated.

Figure 9 Alignment of the DGAT amino acid sequences of *Arabidopsis thaliana* (Ath), *Brassica napus* (Bna), *Perilla fructescens* (Pfr), *Caenorhabditis elegans* (Cel), *Mus musculus* (Mmu), *Rattus norvegicus* (Rno), *Ceropithecus aethiops* (Cea), *Homo sapiens* (Hsa) and two alleles of *Bos taurus* (Bta_1, Bta_2) using PILEUP of the GCG package. Sequences are assembled using BOXSHADE (http://www.isrec.isb-sib.ch:8080/software/BOX_form.html). Numbers on the left indicate amino acid positions. Red letters indicate identical amino acids. Blue letters

indicate conserved amino acids. The red arrows indicate identical lysine residues that might play a role in Acyl CoA binding. The blue arrow indicates conserved amino acids in animal species and in the bovine allele associated with high milk fat content. The lysine to alanine mutation at this position is not conservative. The alanine residue of the allele associated with low milk fat content could have a negative effect on the Acyl CoA binding capacity of DGAT.

Figure 10 Hydrophobicity plot of DGAT as assessed by Kyte-Doolittle analysis (http:// bioinformatics.weizmann.ac.il/hydroph/plot_hydroph.html). Hydrophobic regions are above the horizontal line. a Translated transcript T0 (The effect of the K232A substitution is indicated in red (K, blue; A, red)). b Translated transcript T2 (missing amino acids 230 to 251 of transcript T0).

Figure 11 Detection of the allelic variation at the nucleotide positions 10433 and 10434 of the *DGAT* gene by *Cfr*I-cleavage in a 411 bp PCR product from bovine genomic DNA (primers 1532 and 1636). Cleavage by *Cfr*I is diagnostic for the alanine bearing allele. Panel A, 5% DMSO in PCR reaction; panel B, PCR without DMSO. Panel A, lane 1, lane 6: homozygous for lysine variant; Panel A, lane 2, 4, 5, 7, 8, 9: heterozygous; Panel A , lane 3, 10, 11, 12: homozygous for alanine variant. Panel B, lanes 1 - 11 represent the same animals as lanes 1 - 11 in panel A. Preferential amplification of the lysine variant (nucleotides AA) over the alanine variant (nucleotides GC) prevents the detection of the alanine variant in the heterozygotes.

Figure 12 Haplotypes of *DGAT1* based on nucleotide positions 3343, 10433, 10434, 11030, 11048, 11993 determined by direct sequencing (*A*) and preliminary frequency estimates for the lysine (*dark*) and alanine (*light*) encoding alleles determined by RFLP assay (*B*). Anatolian Black is a breed indigenous of a region known as the site of domestication of the European Bos taurus [Medjugorac, 1994].

Figure 13 (*A*) Distributions of breeding values for milk fat content of Holstein-Friesian (HF), Fleckvieh (FV) and Braunvieh (BV) artificial insemination (AI) bulls born in 1990 or later. Colored areas indicate the range of the breeding values, from

which bulls were chosen for the extreme positive (+, *dark*) and negative (-, *light*) pools for HF (32 per pool), FV (32 per pool) and BV (20 per pool), respectively. HF bulls were selected among 2857 AI bulls. The mean breeding value for milk fat content of the unselected bulls was -0.148, the standard deviation was 0.284. Bulls with breeding values above 0.48 and below -0.68 were selected. The mean breeding values (± standard deviations) of pooled groups were as follows: HF32+, 0.622 ± 0.125; HF32-, -0.771 ± 0.063. FV bulls were selected among 4070 AI bulls. The mean breeding value for milk fat content of the unselected bulls was 0.089, the standard deviation was 0.217. Bulls with breeding values above 0.5 and below -0.3 were selected. The mean breeding values (± standard deviations) of pooled groups were as follows: FV32+, 0.683 ± 0.153; FV32-, -0.454 ± 0.061. BV bulls were selected among 656 AI bulls. The mean breeding value for milk fat content of unselected bulls was 0.006, standard deviation 0.185. Bulls with breeding values above 0.2 and below -0.2 were selected. Mean breeding values (± standard deviations) of pooled groups were as follows: BV20+, 0.424 ± 0.156; BV20-, -0.317 ± 0.096. (*B*, *E*) Consed views of sequencing traces for positions 10430-10437 within the *DGAT1* coding sequence for individual animals (*E*) and DNA pools (*B*). (*C*) Allele frequency shifts. Position of variant and bases are indicated below horizontal axis. Frequencies at position 10433 are determined by genotyping individual animals by sequencing or RFLP assay. Frequencies at position 11030 and 11048 in FV + pool are determined by sequencing. The other frequencies represent estimates from sequence traces (as described in methods). Variable positions 10433 and 10434 are responsible for the K232A substitution. (*D*) Bars represent the frequencies of alleles with 3, 4 5, 6 and 7 repeat units in 5'-region of *DGAT1* in + pool (*dark*) and – pool (*light*) for each breed.

Figure 14 (*A*) Across family test statistic curve for QTL analyses of milk fat content on chromosome 14 for a Fleckvieh granddaughter design. F ratios testing for the presence of a segregating QTL are plotted for given positions along the chromosome. The marker map with distances in cM between markers is shown on the x-axis. Empirical chromosome-wide and genome-wide 1% significance levels achieved via 10,000 permutations are indicated as horizontal lines. (*B*) The bars

show transformed significance levels (log (1/p)) of the test statistic for a segregating QTL present within each family (x-axis). The horizontal line indicates the transformed 1% significance level for a single family after correcting for multiple testing of 20 families. QTL-effects for milk fat content and their respective standard errors are shown on top of the bars for significantly segregating sires. (*C*) Detection of allelic variation at nucleotide positions 10433 and 10434 (K232A) of the *DGAT1* gene by *Cfr*I-cleavage in a 411 bp PCR product from bovine genomic DNA of sire 1 to 16. Cleavage by *Cfr*I is diagnostic for the allele encoding alanine (GC). No DNA samples were available for sires 17 to 20.

Figure 15 Haplotypes of two segregating (*Qq*) bulls. HF: Holstein-Friesian, FV: Fleckvieh. The arrows indicate the homozygous sites, implicating these variants are not causal.

Figure 16 Distribution of breeding values of sons of non segregating sires according to whether or not they have received the lysine alleles from their dams.

The examples illustrate the invention:

Example 1: Preparation of the primers

All primers used in the following procedures were designed using the Primer3 program (www.genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi). Unless indicated directly in the text, primer sequences are listed in Table 1 and Table 2.

Example 2: Radiation hybrid panel mapping

25 ng of genomic DNA from the human-hamster radiation hybrid panel Genbrige 4 (HGMP Resource Center) were amplified with one set of primers specific for the human DGAT gene (forward (1534), 5'-GAGGCCTCTCTGCCCTATG-3'; reverse (1538), 5'-TTTATTGACACCCTCGGACC-3'). PCR was performed on 84 clones of the RH-panel and analyzed by gel electrophoresis (2% agarose). PCR conditions were as follows: 10 µl total volume containing 0.5 µM of each Primer, 200 µM of each dNTP, 1 µl 10xPCR reaction puffer, 1.5 mM $MgCl_2$ and 0.5 U AmpliTaq polymerase (PE Biosystems). The reactions were amplified in a TGradient Thermocycler (Biometra) under following conditions: 1 cycle at 94°C for 3 min, followed by 30 cycles at 95°C for 30 sec, 60°C for 1 min, 72°C for 1 min, followed by 1 cycle at 72°C for 10 min. Positive and negative PCR assays were reported as 1 and 0, respectively, unclear assays as 2. The data were analyzed with a program provided from The Sanger Center (www.sanger.ac.uk/Software/RHserver/RHserver.shtml).

Example 3: Screening of bovine BAC library

Screening was performed by hybridization of high-density filters. A specific PCR product of 565 bp (forward primer (1599), 5'-CGAGTACCTGGTGAGCATCC-3'; reverse primer (1601), 5'-TGTGCACAGCACTTTATTGAC-3') was used as a probe for radioactive screening of the bovine RPCI-41 genomic BAC library (Warren *et al.*, 2000). PCR conditions were as follows: 20 µl total volume containing 0.5 µM of each Primer, 200 µM of each dNTP, 2 µl 10xPCR reaction puffer, 1.5 mM $MgCl_2$ and 1.0 U AmpliTaq polymerase (PE Biosystems). Temperature cycling were as

follows: 1 cycle at 94°C for 3 min, followed by 30 cycles at 95°C for 30 sec, 60°C for 1 min, 72°C for 1 min, followed by 1 cycle at 72°C for 10 min. Probes were labeled with 50 µCi of alpha[^{32}P]dATP using the Megaprime DNA labeling system following the manufacturer protocol (Amersham). Labeled probe was added to the filter in Church buffer and hybridized at 67°C overnight. Filters were washed twice in 2x SSC and once in 0.5x SSC + 1% SDS for 20 minutes at 63°C, respectively. Filters were exposed to Fuji NewRX film at -80°C for 5 h. Positive clones were confirmed by PCR amplification (same primer and conditions as above) and DNA sequencing.

Example 4: Sequencing from BAC-DNA

BAC-DNA was isolated using the QIAGEN Large-Construct Kit (Qiagen) following the manufacturer protocol. In the first step, primers (Table 1) for genomic walking were derived from the known bovine sequence of exon 2 (forward, 1602) and exon 3 (reverse, 1634). In addition to that, a primer (forward, 1632) was derived from the human sequence of exon 1 showing high homology to Cercopithecus aethiops (accession#: AF236018), Mus musculus (accession#: NM_010046), Rattus norvegicus (accession#: AF296131). Further primers were derived from the obtained sequences. Conditions of sequencing reaction were as follows: 150 ng BAC-DNA, 0.4 mM primer and 10 µl BigDye Ready Reaction Mix (PE Biosystems) were combined in a total volume of 25 µl. Temperature cycling were as follows: 1 cycle at 96°C for 5 min, followed by 80 cycles at 96°C for 20 sec, 55°C for 10 sec, 60°C for 4 min. DNA was precipitated with 60% isopropanol, washed with 75% isopropanol, loaded on a 36 cm WTR acrylamid gel (5.5%) on an ABI Prism 377 DNA sequencer. Sequence data were analyzed using the Phred/Phrap/Polyphred/Consed software suite (Nickerson *et al.*, 1997; Ewing and Green, 1998; Ewing *et al.*, 1998; Gordon *et al.*, 1998).

Example 5: Preparing of genomic DNA samples

DNA was prepared from bull semen. After washing with TE buffer (10 mM TrisHCl, 1 mM EDTA), cells were lysed by adding 500 µl PK buffer (20 mM TrisHCl, 4 mM EDTA, 10 mM NaCl), 100 µl SDS (10%), 25 µl DTT (1 M), 60 µl proteinase K (20

mg/ml) and incubated at 50°C overnight. Phenol/chloroform extraction was carried out in 9.5 ml VACUTAINER® tubes (#366510, Becton Dickinson). In the first step 800 µl of phenol/chloroform/isoamylalcohol (25:24:1) was added, mixed thoroughly and centrifuged for 15 min at 2000 g at RT. Traces of phenol were removed by centrifugation after adding 800 µl of chloroform/isoamylalcohol (24:1). DNA was precipitated with ethanol and resuspended in TE buffer. DNA concentration was measured using a fluorometer and adjusted to a concentration of 25 ng/µl. Quality and quantity of DNA was indepently assessed through agarose gel electrophoresis and by performing PCR (primer and conditions as in Screening of bovine BAC library). Only DNA samples showing perfect results in both gel electrophoresis and PCR were used for DNA samples for individual animals and for composing pooled DNA samples.

Example 6: Comparative sequencing

Screening for variations was performed using the DNA samples of the individual animals and the pooled DNA samples in combination with several primer sets (Table 2). Each DNA sample (50 ng) was amplified in 20 µl reactions containing 0.5 µM of each Primer, 200 µM of each dNTP, 1 µl 10xPCR reaction puffer (containing 15 mM $MgCl_2$), 0.5 U HotStar polymerase (Qiagen). Temperature cycles were as follows: 1 cycle at 95°C for 15 min, followed by 35 cycles at 94°C for 1 min, 60°C for 1 min, 72°C for 1 min, followed by 1 cycle at 72°C for 10 min. The PCR amplified fragments were directly purified with the QIAquick PCR purification kit (Qiagen) and analyzed on a 1.5% agarose gel. Conditions of sequencing reaction were as follows: In a total volume of 10 µl was combined 20 ng PCR fragment, 0.5 µM Primer, 4 µl BigDye Ready Reaction Mix (PE Biosystems). Temperature cycling were as follows: 1 cycle at 96°C for 15 sec, followed by 25 cycles at 96°C for 10 sec, 51°C for 5 sec, 60°C for 4 min. DNA was precipitated in 60% isopropanol, washed with 75% isopropanol and run on a 36 cm WTR 5.5% acrylamid gel on an ABI Prism 377 DNA sequencer. Sequence data were analyzed using the Phred/Phrap/Polyphred/Consed software suite (Nickerson *et al.*, 1997; Ewing and Green, 1998; Ewing *et al.*, 1998; Gordon *et al.*, 1998).

Example 7: Estimation of allelic frequencies based on sequencing traces

The amplitude values at the variable positions were extracted from data files ".poly" created by the base calling program phred. The amplitude value for a given base was divided by the normalization factor for that base. The normalized amplitude value of pooled DNA (P) was compared with the amplitude value of homozygous (Ho) or heterozygous (He) individual animals or monomorphic pools. Averages were taken when amplitude values were available for more than one animal. Frequency estimates (F) were obtained by the following calculations: F = P / Ho or F = (0.5 x P) / He.

Example 8: RFLP-Analysis of PCR-Fragments

The genotyp of an individual or group of animals was tested by the use of RFLP-analysis. Detection of allelic variation at the nucleotide positions 10433 and 10434 of the *DGAT* gene was effected by *Cfr*I-cleavage in a 411 bp PCR product from bovine genomic DNA (primers 1532 and 1636). Cleavage by *Cfr*I is diagnostic for the alanine bearing allele. The result of a test is shown in figure 11. PCR reactions were carried out in the presence (panel A) or absence (panel B) of 5 % DMSO. PCR-products were isolated following common protocols as known by a person skilled in the art and incubated with the restriction endonuclease *Cfr*I under conditions in line with manufactures advice. Figure 11 shows in panel A, lane 1 and lane 6 samples, which are homozygous for lysine variant. In lane 2, 4, 5, 7, 8, 9 of panel A samples with heterozygous genotype are shown. Furthermore, lane 3, 10, 11, 12: show samples which are homozygous for alanine variant. In panel B, lanes 1 - 11 samples of the same animals as shown in lanes 1 - 11 of panel A are displayed. Preferential amplification of the lysine variant (nucleotides AA) over the alanine variant (nucleotides GC) prevents the detection of the alanine variant in the heterozygotes.

Example 9: Direct sequencing reveals at least 8 haplotypes of DGAT1

Direct sequencing in animals belonging to different breeds of Bos taurus taurus and Bos taurus indicus as well as in animals of *Bos grunniens* (yak) and *Bubalus*

bubalus (water buffalo) at 6 of the variable nucleotide positions allowed to derive at least 8 haplotypes (Fig. 12). Lysine encoding haplotypes are present in yak and water buffalo. Thus, the lysine encoding variant is likely to represent the ancestral state of *DGAT1*. However, the K232A substitution is likely to have taken place early in the history of domesticated cattle or even before domestication as surmised by the presence of the alanine variant in the "old" cattle breed Anatolian Black. An RFLP assay was applied to obtain preliminary estimates on the frequency of the lysine and alanine encoding alleles in several cattle breeds and species of *Bovinae* subfamily (Fig. 12).

Example 10: Distribution of breeding values for milk fat content

The frequencies at 6 variable positions in the pools of animals with high and low breeding values for milk fat content, respectively, are visualized in Fig. 13. There are distinct differences for the Fleckvieh and Holstein-Friesian-Friesian breeds in the frequencies between the groups of animals with low and high breeding values for milk fat content, respectively, indicating association between variation in the *DGAT1* gene and genetic variation of the milk fat content. The most extreme differences are between the "low" and "high" pools in the Holstein-Friesian breed. In both breeds, the lysine encoding variant is more frequent in animals with high breeding values for milk fat content. The lysine encoding allele is also slightly less more frequent in the Braunvieh animals from the high end of the distribution of the milk fat content breeding values.

Example 11: Across family test statistic curve for QTL analyses of milk fat content on chromosome 14 for a Fleckvieh granddaughter design

Another argument for *DGAT1* (or linked loci) being responsible for the QTL-variation on chromosome 14 is provided by the results obtained from interval QTL mapping in theFleckvieh breed using a half-sib design, the so called granddaughter design. The test statistic for the presence of a QTL along chromosome 14 (Fig. 14) indicates the

most likely position of the QTL close to marker *ILSTS039*. Evidence was highly significant for segregation of the QTL in two out of 20 families (Fig. 14). Estimates of QTL effects for milk fat content in the segregating families were found to be 0.313 ± 0.070 and 0.409 ± 0.064, respectively. These effects greatly exceed the genetic standard deviaion of 0.2 in the Fleckvieh population. The genotypes at the predicted K232A substitution determined by an RFLP assay are compatible with the heterozygous status of the segregating (*Qq*) sires and homozygosity of the alanine encoding variant of the non-segregating (most likely *qq*) sires (Fig. 14).

Example 12: Haplotypes of two segregating (Qq) bulls

Direct sequencing of *DGAT1* from DNA and determining the repeat number of the 5'-VNTR in the two segregating bulls and some of their progeny allowed to derive the haplotypes based on the genotypes of the homozygous progeny. The lysine encoding variant is present on two different haplotypes, i.e. the only lysine bearing haplotype in Holstein-Friesian and a Fleckvieh-specific haplotype (Fig. 12, Fig. 15). This could indicate that a lysine encoding allele has been introduced into Fleckvieh from Holstein-Friesian. Pedigree analysis indeed shows that the great- grandfather of bull 899 was a purebred Holstein-Friesian sire while there is no indication of Holstein-Friesian ancestry for bull 705. Three of the 7 variable positions that make up the haplotypes are homozygous in *Qq* bull 705 (Fig. 15). Thus they can be excluded to be causal. The variants responsible for the K232A polymorphism, however, are heterozygous in both *Qq* bulls.

Example 13: Distribution of breeding values of sons of non segregating sires

An independent association study was carried out based on the breeding values for milk fat content of the sons of non segregating sires. These sons were grouped according to the allelic variant (lysine or alanine) which they have received from

their dams as determined by the RFLP assay. The respective means of breeding values were compared after correction of half the sire's breeding value (Fig. 16). The difference of +0.265 for the group carrying the lysine variant was highly significant ($P < 0.0001$) and strongly supports the size of the gene substitution effect found via linkage analysis. It is also in agreement with the results of the association study presented above. Since the dams can be considered to represent a random sample of the Fleckvieh population with regard to milk fat content, the association involving the sons of non segregating sires is not likely to be confounded by admixture.

Example 14: Mast Experiment "Dummersdorf" – Evaluation of DGAT

Objective: Impact of DGAT for intramuscular fat content.
Material:
The experiment is based on data obtained from 56 slaughtered fattened animals of both gender of the races Deutsche Holstein Friesian (n=29) and Charolais (n=27). IMF-values of MLD (IMF_MLD) and Bratenstück [bitte übersetzen] (IMF_SEMI) and the exchange of K232A in DGAT were determined. The allelic frequency of the lysine variant, in both tested samples, were estimated as 11% for Charolais and 45% for Holstein Friesian.

Statistical analysis:

The statistical analysis was established by using the method of least squares which is part of the program SAS (Version 8.02). The analysis of the total material was based on the model:

$$Y_{ijklm} = Race_i + Father_j\,(Race_i) + Gender_k + DGAT\text{-}Genotype_l + e_{ijklm}$$

In another analysis, the data was evaluated for each race separately, wherein the effect of the race of the above-indicated model is left out. By employing the variance analysis, the contribution of the individual factors for the establishment of the IMF

properties was tested. Moreover, least square means were calculated for the specific genotypes, the differences of which represent an estimate reflecting the differences between these genotypes.

Results:

All experiments showed a significant gender-impact. Table 13 summarizes the F- and p-values and levels of significance (n.s: not significant; *: $p<0.05$) of the variance analysis for the effect of DGAT genotypes. The results indicate a significant impact of DGAT on IMF_SEMI and no indication of an impact on IMF_MLD. The increased F-values of Holstein Frisian in comparison with Charolais (when data was evaluated for each race separately) may rest on the fact that a homozygous lysine variant never occurred in Charolais. From analyses on the TG locus a recessive inheritance is suggested, wherein Alanin is dominant over Lysine, thus, preventing the detection of the effect on IMF in Charolais.

Table 14 summarizes the least square means and their standard error. The predominance of L/L genotypes over L/A and A/A, as evident from the analysis, amounted to 1.6% percent in IMF_SEMI. When analyzed separately, on average a similar difference is found in Holstein Frisian. However in the latter case, the results for the genotypes L/A and A/A are less uniform and have to be discussed with caution since they are associated with a high standard error. The differences observed are of a magnitude which are likely to be only possible in extremely fastened animals. The resulting high variability of starting material may also be the reason for a lack of statistical support of the large differences in IMD_MLD of Hostein Friesian.

Tables:

Table 1: Primers used for sequencing of BAC-DNA

Location in *DGAT*	#	Direction	Sequence
5'end	1738	reverse	5'-TGATGCCTACCTAAGCTCTACC-3'
5'end	1739	reverse	5'-TTTAGGGTCTGAGCCACCAG-3'
5'end	1728	reverse	5'-TCCCGACTCTTTGTGACTCC-3'
5'end	1734	reverse	5'-TGGATTGCAAAGTCCTGTCC-3'
5'end	1717	reverse	5'-CAGGAAGGGCCTCTGTACC-3'

5'end	1716	reverse	5'-ACAGCTGGAGTGAGGACACC-3'
5'end	1710	reverse	5'-CCCTCAGCGCTAGGACTC-3'
5'end	1709	reverse	5'-TGTCTTGGAGTAGCGTGTGG-3'
5'end	1706	reverse	5'-AGGCCCCCACAGTAGACAAG-3'
5'end	1705	reverse	5'-ACGGTCGTGCTCTGTGAAC-3'
5'end	1699	reverse	5'-CCCTTGTCCCGCTCTATAAAC-3'
5'end	1698	reverse	5'-CGCGCATACCTTTGTAGTCC-3'
5'end0	1697	reverse	5'-CGCCTCTACTACGCCACTG-3'
Exon 1	1632	forward	5'-GCCACTGGGAGCTGAGG-3'
Intron 1	1681	reverse	5'-ACAGCTGTGCACCAAGGTC-3'
Intron 1	1680	forward	5'-TGGCTGCTCTAGGGTCAAAG-3'
Intron 1	1693	forward	5'-ATCTTCACTGGGTGCTGTGG-3'
Intron 1	1694	forward	5'-CTGCTCCTGTCCTGTTGATG
Intron 1	1696	reverse	5'-AGCCACCTCATGCTACAACC-3'
Intron 1	1695	reverse	5'-GCCCTCTTCTTCATGACTCTG-3'
Intron 1	1679	reverse	5'-GGCCACCATTCAAACCAC-3'
Exon 2	1602	forward	5'-GAATTGGTGTGTGGTGATGC-3'
Intron 2	1675	reverse	5'-GGTAGGGTCCCAGGGTACG-3'
Intron 2	1673	forward	5'-GCCACACTCTGCAGGACTC-3'
Intron 2	1674	reverse	5'-CAGTCCTGCTCCCTCCAG-3'
Intron 2	1671	reverse	5'-TGACAGGCTCAGAGATGCAG-3'
Intron 2	1660	reverse	5'-AGCCCCAGTGAAGTCCAAG-3'
Exon 3	1634	reverse	5'-TAGAAATAACCGTGCGTTGC-3'
Exon 4	1633	reverse	5'-ACCTGGATGGGGTCCAC-3'
3'end	1593	forward	5'-GTGGGTGTTGGACTGCTTTG-3'
3'end	1711	forward	5'-CCATGCTCTGGAAACCCTAC-3'
3'end	1729	forward	5'-TCAGCAGGTAGTTGGGTGTG-3'
3'end	1730	forward	5'-GAAACCCTGAGGCTGTGC-3'
3'end	1732	forward	5'-CCCACCTGGTCCTCTAGTGC-3'
3'end	1733	forward	5'-CCAGGAGGCTCCAGTGTG-3'
3'end	1737	forward	5'-GTTCTGAGCCCGTCAGCAG-3'
3'end	1739	forward	5'-TTTAGGGTCTGAGCCACCAG-3'

Table 2: Primers used for PCR and comparative sequencing of genomic DNA

Location in *DGAT*	Forward primer		Reverse primer	
	#	Sequence	#	Sequence
Exon 1	1701	5'-CGCGTTGGGTGTCAGC-3'	1681	5'-ACAGCTGTGCACCAAGGTC-3'
Exon 2	1702	5'-TGGCTTCTGCAGTGGACTC-3'	1675	5'-GGTAGGGTCCCAGGGTACG-3'
Exon 3-4	1670	5'-GTGGCTGACAGCGTTATGTC-3'	1676	5'-GTTCAGGCCCAGATCAGC-3'
Exon 4-6	1614	5'-TATGGCATCCTGGTGGAC-3'	1617	5'-AGTGATAGACTCGAGGAGAAAGG-3'
Exon 6-7	1616	5'-GGAGCTCTGACGGAGCAG-3'	1635	5'-GTTGACGTCCCGGTAGGAG-3'
Exon 7-9	1532	5'-GCACCATCCTCTTCCTCAAG-3'	1636	5'-GGAAGCGCTTTCGGATG-3'
Exon 9-11	1618	5'-CCCTGTGCTACGAGCTCAAC-3'	1678	5'-CACAGCTGGCTCCCTCAG-3'
Exon 11-14	1638	5'-GCCATCCAGAACTCCATGA-3'	1640	5'-CAGGGATGTTCCAGTTCTGC-3'
Exon 13-16	1677	5'-GAGTTCTACCGGGACTGGTG-3'	1641	5'-ATCATGCCGGTGAAGGC-3'
Exon 16-17	1599	5'-CGAGTACCTGGTGAGCATCC-3'	1601	5'-TGTGCACAGCACTTTATTGAC-3'
5'end	1755	5'-AGAAATGGGAAGTGCAGACC-3'	1738	5'-TGATGCCTACCTAAGCTCTACC-3'
5'end	1754	5'-CAGGGTGGGATCACCTGAG-3'	1734	5'-TGGATTGCAAAGTCCTGTCC-3'
5'end	1753	5'-GGTGGATGACGGGTAGAGG-3'	1716	5'-ACAGCTGGAGTGAGGACACC-3'
5'end	1721	5'-TGAGGCCCTGATCTCTCAAC-3'	1709	5'-TGTCTTGGAGTAGCGTGTGG-3'
5'end	1722	5'-AAGGGGATACTCCTGATCCAC-3'	1706	5'-AGGCCCCCACAGTAGACAAG-3'
5'end	1723	5'-TCTGCAGATGAAGGCAGAAG-3'	1698	5'-CGCGCATACCTTTGTAGTCC-3'
3'end	1711	5'-CCATGCTCTGGAAACCCTAC-3'	1718	5'-GCGGCAGAGCCAGTAGAG-3'
3'end	1729	5'-TCAGCAGGTAGTTGGGTGTG-3'	1756	5'-CTCCCTGTCTGTTCCTCCTG-3'
Intron 1	1866	5'-GACACCTGGTGCGTCCTTC-3'	1867	5'-GAGGGGAGCATTTCCCAATC-3'
Intron 1	1868	5'-TACCCCCACAGACTGTCCTC-3'	1679	5'-GGCCACCATTCAAACCAC-3'
Intron 2	1602	5'-GAATTGGTGTGTGGTGATGC-3'	1674	5'-CAGTCCTGCTCCCTCCAG-3'
Intron 2	1673	5'-GCCACACTCTGCAGGACTC-3'	1671	5'-TGACAGGCTCAGAGATGCAG-3'
Intron 2	1672	5'-TGGTAAGCTGGCTGGTTAGG-3'	1634	5'-TAGAAATAACCGTGCGTTGC-3'

Table 3: Results of PCR analysis of Genebridge 4 (GB4) hamster-human radiation hybrid panel

No.	Cell line	PCR assay [a]
1	4A4	0
2	4A5	2
3	4AA5	1
4	4AA7	0
5	4B2	2
6	4B3	0
7	4B9	2
8	4BB1	0
9	4BB6	0
10	4BB8	1
11	4BB10	2
12	4BB12	2
13	4C3	1
14	4C11	0
15	4CC8	0
16	4D1	0
17	4D7	0
18	4DD2	0
19	4DD5	1
20	4DD8	0
21	4E2	1
22	4E4	0
23	4E6	0
24	4E11	0
25	4F6	1
26	4F7	1
27	4F13	0
28	4G1	0
No.	Cell line	PCR assay
29	4G5	0
30	4G6	0
31	4G7	0
32	4G11	1
33	4H1	0
34	4H8	0
35	4H9	1
36	4H12	0
37	4I1	0
38	4I4	1
39	4J2	0
40	4J5	0
41	4J9	0
42	4K5	0
43	4K7	1
44	4K8	2
45	4K9	0
46	4K12	1
47	4L3	1
48	4L4	0
49	4L6	0
50	4M4	0
51	4M5	1
52	4N3	0
53	4N5	0
54	4N6	0

55	4N7	0
56	4N12	1
57	4O5	0
58	4O10	2
59	4P2	0
60	4P9	0
61	4P11	0
62	4Q2	1
63	4Q4	0
64	4R1	0
65	4R2	0
66	4R3	0
67	4R5	0
68	4R6	0
69	4R10	1
70	4R12	2
71	4S3	1
72	4S6	0
73	4S10	2
74	4S12	0
75	4T3	0
76	4T4	0
77	4T10	0
78	4T11	0
79	4U1	1
80	4U3	2
81	4V2	1
82	4V3	0
83	4V7	0
84	4V8	0
85	4W1	0
86	4Y4	0
87	4Y8	0
88	4Y9	0
89	4Z5	0
90	4Z6	0
91	4Z9	1
92	4Z11	0
93	4Z12	0

No.	Cell line	PCR assay

(a) 0, negative; 1, positive; 2, not assayed

Table 4: Bovine ESTs identified in the EST database using the human *DGAT* mRNA sequence (accession XM_005135) as input for BLASTN (Continued)

Accession	Size (in bp)	Source of mRNA	Position in bovine *DGAT*[(a)]
AW446908	*479*	*pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary*	*256-780 (exon 2-9)*
AW483961	*205*	*pooled tissue from day 20 and day 40 embryos*	*1594-1745 (3'UTR)*
AW486026	*385*	*pooled tissue from day 20 and day 40 embryos*	*1336-1720 (exon17-3'UTR)*
AW652329	*542*	*pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary*	*990-1530 (exon 13-3'UTR)*
BE664362	*415*	*pooled tissue from day 20 and day 40 embryos*	*1321-1735 (exon17-3'UTR)*
BE753833	*422*	*pooled tissue from testis, thymus, semiten-dono sus muscle, longissimus muscle, pancreas, adrenal, and endometrium*	*1369-1745 (exon17-3'UTR)*
BE664357	*456*	*pooled tissue from day 20 and day 40 embryos*	*1321-1745 (exon17-3'UTR)*
BE900091	*527*	*adipose tissue*	*1097-1561 (exon14-3'UTR)*
BE751071	*475*	*pooled tissue from testis, thymus, semiten-dono sus muscle, longissimus muscle, pancreas, adrenal, and endometrium*	*1087-1560 (exon14-3'UTR)*
AW446985	*485*	*pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary*	*594-1143 (exon 7-11)*
AW326076	*141*	*pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary*	*703-772 (exon 8-9)*
BE486748	*174*	*mammary tissues at eight physiological, devel opmental, and disease states*	*906-986 (exon 11-12)*

(a) Base 1 = first base of start codon

Table 5: Exon-intron structure of the bovine DGAT gene

Exon	Position in bovine *DGAT*[a]	Size (bp)	5'-splice donor[b]	Intron	Size (bp)	3'-splice acceptor[b]
1	1-191	191	CCTGAG**gt**agcg	1	3617	ctcc**ag**GTGTCA
2	192-279	88	ATGCTG**gt**acgt	2	1944	tcgc**ag**ATCTTA
3	280-320	41	CATCAA**gt**gagt	3	79	ctgc**ag**GTATGG
4	321-406	86	TCATTG**gt**gagc	4	92	cctc**ag**TGGCCA
5	407-459	53	GCCGTG**gt**aagc	5	215	cccc**ag**GGAGCT
6	460-565	106	CTCCAG**gt**gggc	6	89	ccac**ag**TGGGCT
7	566-679	114	AGGCTG**gt**gagg	7	100	tcgt**ag**CTTTGG
8	680-754	75	ACCGCG**gt**gagg	8	70	ttcc**ag**ATCTCT
9	755-858	104	GAGATG**gt**gagg	9	90	cccc**ag**CTGTTC
10	859-897	39	CAGCAG**gt**acgt	10	60[c]	ttgc**ag**TGGATG
11	898-939	42	TTCAAG**gt**gagc	11	73	ccac**ag**GACATG
12	940-984	45	CTGGCG**gt**gagt	12	74	ccac**ag**GTCCCC
13	985-1097	113	CTGGTG**gt**gggt	13	87	ccgc**ag**GAACTC
14	1098-1163	66	CATCAG**gt**gggt	14	86	ccgc**ag**ACACTT
15	1164-1251	88	CACGAG**gt**cagt	15	81	cctc**ag**TACCTG
16	1252-1314	63	GCGCAG**gt**gagc	16	72	cccc**ag**ATCCCG
17	1315-1470	156				

(a) Base 1 = first base of start codon

(b) Exon sequences are indicated in upper case letters, intron sequences in lower case letters. The consensus splice site sequences are in boldface.

(c) Intron 10 contains a $(G)_n$ stretch that could not be resolved by sequencing.

Table 6: Panel of individual animals and animals belonging to a pool

	Lab. no.	Herdbook no.	Breed	Sub-species [a]
individual animals	FV19	7620	Simmental	*taurus*
	FV27	25100	Simmental	*taurus*
	FV28	50148	Simmental	*taurus*
	SB26	790580	Simmental	*taurus*
	SB37	102430	Simmental	*taurus*
	SB45	252006	Simmental	*taurus*
	AN1		Angus	*taurus*
	KE2		Kerry	*taurus*
	SA4		Sahiwal	*indicus*
	HA8		Hariana	*indicus*
SBpool	SB 2	102399	Holstein-Friesian	*taurus*
	SB 9	790121	Holstein-Friesian	*taurus*
	SB 13	790223	Holstein-Friesian	*taurus*
	SB 14	790253	Holstein-Friesian	*taurus*
	SB 22	790510	Holstein-Friesian	*taurus*
	SB 33	790361	Holstein-Friesian	*taurus*
	SB 41	790062	Holstein-Friesian	*taurus*
	SB 43	790183	Holstein-Friesian	*taurus*
	SB 44	102350	Holstein-Friesian	*taurus*
	SB 47	102315	Holstein-Friesian	*taurus*

(a) Bos taurus taurus or Bos taurus indicus

Table 7: Composition of DNA pools: Fleckvieh (Bavarian Simmental) breed

Pool [a]		Lab. no.	Herdbook no.	Name	Breeding value
FVpool32+	FVpool12+	901	194100	HASTROL	0.83
		902	195260	PROLAP	0.78
		903	50223	LABTON	0.77
		906	39910	RAPID	0.75
		907	169044	HAGENT	0.74
		910	178317	LOCANDA	0.71
		911	165011	HAGER	0.70
		912	7889	ROLAND	0.70
		1066	1146	LOMBARD	0.70
		913	34380	ALPAN	0.69
		914	187217	HALLSTRAS	0.69
		916	60535	LAMBADA	0.69
		917	60250	PLANSEE	0.69
		918	54474	PROMO	0.69
		919	172162	LOMB	0.68
		920	184506	LOMO	0.68
		921	169042	HAGSON	0.67
		922	172174	LOMBOLO	0.66
		923	178308	LORETTO	0.66
		924	165010	HAGEL	0.65
		925	22153	RALBIT	0.65
		926	645073	ZEPTER	0.65
		927	60527	ALPIN	0.64
		930	34554	STREUSAND	0.63
		932	187049	HALLERTAU	0.62
		933	21784	UTNACH	0.62
		935	187138	HALBEM	0.59
		936	175061	HALLEM	0.59
		937	191053	HATARI	0.59
		939	53535	GAST	0.58
		940	191045	RODOS	0.57
		942	50246	FODA	0.56
FVpool32-		1019	45432	HONER	-0.31
		1021	53381	PRO	-0.31
		1023	178075	RAVELLI	-0.31
		1025	191283	WALTL	-0.31
		1026	39733	WESPE	-0.31
		1029	68130	RAUDI	-0.33
		1032	27876	HERMANUS	-0.34
		1033	21971	HOPPE	-0.34
		1034	22043	HOPURG	-0.34
		1035	60552	HUMBACH	-0.34
		1036	68030	ZAR	-0.34

	1038	22093	PRONER	-0.35
	1039	184256	RAUWOLF	-0.35
	1040	187114	RIVA	-0.35
	1043	184280	JUL	-0.36
	1046	53487	BONWEIN	-0.37
	1047	53493	PREUS	-0.37
	1048	68175	RAMSES	-0.37
	1049	53607	ROTWEIN	-0.37
	1050	53625	PRODOMO	-0.38
	1051	176156	RAFAEL	-0.38
	1053	27848	WIND	-0.39
	1054	68040	HIRTE	-0.41
	1055	53517	WICHT	-0.41
	1056	7787	WHISKY	-0.43
	1058	176009	FREDL	-0.45
	1060	39860	WIM	-0.46
	1061	53460	WINZER	-0.46
FVpool12-	1062	53293	ZECHER	-0.46
	1063	27847	RENOIR	-0.47
	1064	68195	RASTER	-0.51
	1065	27851	WICKY	-0.51

(a) The bulls were selected among 4070 artificial insemination bulls born 1990 and later. The mean breeding value fat % of the unselected bulls was 0.089, the standard deviation 0.217. Bulls with breeding values greater 0.5 (N = 154, mean = 0.646 ± 0.117) and smaller -0.3 (N = 89, mean = -0.380 ± 0.062) were selected. DNA samples could be obtained from 48 bulls on the positive side (mean = 0.647 ± 0.079) and 36 bulls on the negative side (mean = - 0.381 ± 0.079). The mean breeding values (± standard deviations) of the pooled groups were as follows: FVpool12+, 0.729 ± 0.045; FVpool32+, 0.669 ± 0.063; FVpool32-, -0.381 ± 0.059; FVpool12-, -0.445 ± 0.042

Table 8: Composition of DNA pools: Braunvieh (Brown Swiss) breed

Pool [(a)]	Lab. no.	Herdbook no.	Name	Breeding value
BVpool20+	909	78780	BREILORI	0.73
	929	79030	BREICON	0.63
	943	340530	EURO	0.54
	951	79195	VINCOL	0.50
	952	79115	EMOZ	0.47
	953	348544	STRIFMAN	0.46
	954	78475	DOTRAY	0.45
	955	348105	BRAY	0.44
	956	349447	BREIMORY	0.42
	957	78635	DOTION	0.40
	959	77888	ROMEIS	0.38
	961	348247	BREIZ	0.37
	962	348591	STRIZIN	0.37
	964	349569	HUCNOS	0.35
	965	72695	DOLEIN	0.34
	966	340573	BREISAD	0.33
	967	340015	STRELE	0.32
	968	78980	EMPIKT	0.31
	971	79080	RELVIN	0.31
	972	78880	BAYDOT	0.29
BVpool20-	1004	78225	DOBROY	-0.22
	1006	78200	VISTAR	-0.22
	1007	348215	CREVIN	-0.24
	1008	72625	TRALAS	-0.24
	1009	348607	VIVAT	-0.24
	1011	72680	BAGAT	-0.27
	1012	72470	SIRAY	-0.27
	1014	72930	PETOS	-0.29
	1015	78090	SIMPUR	-0.30
	1017	78470	BARI	-0.31
	1018	78840	BLESTRI	-0.31
	1024	78860	RENZ	-0.31
	1027	78560	JETSTRI	-0.30
	1028	72490	JUP	-0.30
	1030	85550	RESTOR	-0.30
	1037	78015	DUKE	-0.40
	1042	78695	CRAUTS	-0.40
	1044	348104	PETMAN	-0.40
	1045	340010	BAY	-0.40
	1057	78155	JARGI	-0.40

(a) The bulls were selected among 656 artificial insemination bulls born 1990 and later. The mean breeding value "fat %" of the unselected bulls was 0.006, the standard deviation 0.185. Bulls with

breeding values greater 0.2 (N = 84, mean = 0.325 ± 0.108) and smaller -0.2 (N = 56, mean = -0.334 ± 0.101) were selected. DNA samples could be obtained from 54 bulls on the positive side (mean = 0.316 ± 0.111) and 22 bulls on the negative side (mean = - 0.306 ± 0.055). The mean breeding values (± standard deviations) of the pooled groups were as follows: BVpool20+, 0.421 ± 0.113; BVpool20-, -0.305 ± 0.057.

Table 9: Variable positions in and around *DGAT* and genotypes of individual animals

		Animals									
Position	**Variation**	**FV19**	**FV27**	**FV28**	**SB26**	**SB37**	**SB45**	**AN1**	**KE2**	**SA4**	**HA8**
1465-1554	4, 5, 6 [a]	4,4	4,4	4,4	5,5	5,6		5,6		4,4	5,6
3343	C - G	CC	GC	CC	CC	CC	CC	CC		CC	CC
3399	T - G	TT	TT	TT	TT	TT	TT	TT		GG	TG
7232	A - G	AA	AA	AA	GG	AA	AA	AA		GG	GG
8567	A - G				AA						
8607	G - A				GG						
9284	T – C [b]										
10147	A - C	AA	AA	AA	AA	AA	AA	AA		CC	AA
10433	G - A	GG	GG	GG	AA	AG	AG	GG	GG	AA	AA
10434	C - A	CC	CC	CC	AA	CA	CA	CC	CC	AA	AA
10508-10512	G5 - G6	G5G5	G5G5	G5G5	G5G5	G5G5	G5G5	G5G5	G5G5	G5G5	G5G6
ca. 10800	PCR [c]	-	-	-	+	+	+	+	+/-	+	+
11030	G - A	GG	GG	GG	AA	AG	AG	GG	GG	GG	AA
11048	C - T	TT	TT	TT	CC	CT	CT	TT	TT	CC	CC
11993	T - C	TT	TT	TT	CC	TC	TC	TT	TT	TT	TT
12005	A - C	AA	AA	AA	AA	AA	AA	AA	AA	CC	AA
12036	T - C	TT	TT	TT	TT	TT	TT	TT	TT	CC	TT
12056	A - G	AA	AA	AA	AA	AA	AA	AA	AA	GG	AA
12136	G - A	GG	GG	GG	GG	GG	GG	GG	GG	AA	GG
13309	G - Cb										

(a) Number of repeats (AGGCCCCGCCCTCCCCGG)

(b) Detected in pooled DNA (see Table 8)

(c) Variable PCR amplification (+, PCR product; -, no or very weak PCR product)

Table 10: Repeat at position 1465-1554 and genotypes of pooled samples

4,4 [a]	4,5 [a]	5,5 [a]
FV12-	FV12+	
FV32-	FV32+	
	BV20-	BV20+

(a) Number of repeats (AGGCCCCGCCCTCCCCGG)

Table 11: Allelic frequencies estimated from sequencing traces of pooled samples

Position [a]	Exchange	SBpool	FV12+	FV12-	FV32+	FV32-	BV20+	BV20-
3343	C – G	1	1	0.79	1	0.70	1	0.82
8567	A – G	n.d.	n.d.	n.d.	0.42	0	n.d.	n.d.
8607	G – A	n.d.	n.d.	n.d.	0	0.49	n.d.	n.d.
9284	T – C	n.d.	n.d.	n.d.	0.54b	0.92d	0.90b	1b
10433	G – A	n.d.	0.39 [b]	1b	0.46b	1	0.90b	1b
10434	C – A	n.d.	0.36b	1b	0.41b	1	0.93b	1b
11030	G – A	n.d.	0.68b	1b	0.64b	1	1b	1b
11048	C – T	n.d.	0.48b	0.20b	0.48b	0.26d	0b	0b
11993	T – C	0.61	0.64	1	0.65	1	1	1
130309	G – C	n.d.	n.d.	n.d.	0.39	1	1	n.d.

(a) Only positions with single base exchanges and that are variable within *Bos taurus taurus*

(b) 5% DMSO in PCR

Table 12: Genotypes of individual animals

Pool	Lab #	Breeding value	Position (base) 10433 (A) [a]	10434 (A) [a]	11030 (A) [a]	11048 (C) [a]
FV12p+	901	0.83	1	1	0	0
	902	0.78	0	0	-	-
	903	0.77	1	1	0	0
	906	0.75	2	2	2	2
	907	0.74	1	1	0	1
	910	0.71	1	1	0	0
	911	0.70	1	1	0	1
	912	0.70	1	1	1	1
	1066	0.70	1	1	0	2
	913	0.69	1	1	0	1
	914	0.69	0	0	0	0
	916	0.69	2	2	1	2
Average / Frequency			0.5%	0.5%	0.18%	0.45%
FV32p+	917	0.69	2	2	0	1
	918	0.69	1	1	0	1
	919	0.68	1	1	0	1
	920	0.68	0	0	0	1
	921	0.67	0	0	0	0
	922	0.66	1	1	0	-
	923	0.66	0	0	0	1
	924	0.65	1	1	0	1
	925	0.65	1	1	1	1
	926	0.65	0	0	0	2
	927	0.64	1	1	1	1
	930	0.63	1	1	1	1
	932	0.62	2	2	0	1
	933	0.62	2	2	1	0
	935	0.59	1	1	0	1

936	0.59	1	1	0	1
937	0.59	1	1	0	1
939	0.58	1	1	1	1
940	0.57	0	0	0	1
942	0.56	1	1	0	1
Average / Frequency		0.47%	0.47%	0.15%	0.94%

(a) 0, 1, 2, number of indicated allele; - assay failure

Table 13: F- and p- values of the variance analysis

Race	IMF_MLD		IMF_SEMI	
	F-Vaule	Sig.	F-Value	P
Total	0,19	0,827 n.s.	3,47	0,040*
Holstein-Friesian	0,36	0,704, n.s.	5,35	0,013*
Charolais	0,15	0,703, n.s.	1,13	0,301, n.s.

Table 14:Least square means and standard error

animals	IMF_MLD		IMF_SEMI	
	LSM +/- s.e.		LSM +/- s.e.	
gesamt				
L/L	5,57	0,99	3,95	0,59
L/A	5,05	0,49	2,35	0,29
A/A	4,88	0,41	2,35	0,24
Holstein-Friesian				
L/L	7,07	1,04	4,33	0,53
L/A	6,14	0,61	2,39	0,31
A/A	6,08	0,82	3,04	0,41
Charolais				
L/A	3,80	0,62	2,46	0,50
A/A	3,53	0,32	1,85	0,26

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CLAIMS

1. A nucleic acid molecule encoding a bovine acyl CoA:diacylglycerol transferase (*DGAT*) contributing to or indicative for low fat content of milk and to low meat marbling (intramuscular fat content) wherein said nucleic acid molecule is selected from the group consisting of:
   (a) a nucleic acid molecule having or comprising the nucleic acid sequence of SEQ ID NO: 1;
   (b) a nucleic acid molecule comprising the coding sequence of the polypeptide of SEQ ID NO: 2;
   (c) a nucleic acid molecule the complementary strand of which hybridizes under stringent conditions to the nucleic acid molecule of (a) or (b), wherein said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 1) a guanine and a cytosine residue; and
   (d) a nucleic acid molecule the complementary strand of which hybridizes under stringent conditions to the nucleic acid molecule of (a) or (b), wherein said nucleic acid molecule has at the *DGAT* gene (SEQ ID NO: 1) position
      (i) 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine;
      (ii) 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine, and 11093 a thymine; or
      (iii) 3343 a guanine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine and 11093 a thymine.

2. The nucleic acid molecule of claim 1 which is mRNA, genomic DNA (gDNA) or cDNA which is derived from said mRNA by reverse transcription of said mRNA.

3. The nucleic acid of claim 2, wherein said gDNA is a gene.

4. A fragment of the nucleic acid molecule of any of claims 1 to 3 having at least 14 nucleotides wherein said fragment comprises nucleotide position 10433 and 10434 of SEQ ID NO: 1.

5. A nucleic acid molecule which is complementary to the nucleic acid of any of claims 1 to 4.

6. A vector comprising the nucleic acid molecule of any one of claims 1 to 5.

7. The vector of claim 6 comprising regulatory elements for expression of said nucleic acid molecule.

8. A primer or primer pair, wherein the primer or primer pair hybridize under stringent conditions to the nucleic acid molecule of any of claims 1 to 5 comprising nucleotide position 10433 and 10434 of SEQ ID NO: 1 or the complement strand thereof.

9. A host cell which contains the expression vector of claim 7.

10. A method for production of a functional bovine *DGAT* or a functional fragment thereof comprising:
    (a) culturing the host cell of claim 9 containing the expression vector which comprises the nucleic acid molecule of any of claims 1 to 3 under conditions allowing the expression of the encoded polypeptide; and
    (b) collecting the polypeptide from the culture.

11. A functional bovine *DGAT* polypeptide or a functional fragment thereof encoded by a nucleic acid molecule according to any of claims 1 to 3 or produced by the method of claim 10.

12. An antibody which binds to an epitope of the polypeptide or fragment of SEQ ID NO: 2 the epitope comprising a alanine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 4 having a lysine at position 232.

13. An antibody which binds to an epitope of the polypeptide or fragment of SEQ ID NO: 4 the epitope comprising a lysine at position 232 but not to a polypeptide or a fragment of SEQ ID NO: 2 having a alanine at position 232.

14. A transgenic, non-human animal comprising at least the nucleic acid molecule of any of claims 1 to 3 or 5.

15. The transgenic, non-human animal of claim 14 wherein said animal belongs to cattle.

16. A method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling comprising analyzing the nucleic acid of a sample comprising the gene encoding *DGAT* or a corresponding mRNA for nucleotide polymorphisms which are connected with said predisposition.

17. The method of claim 16, wherein the nucleic acid molecule analyzed is the nucleic acid molecule of claim 1.

18. The method of claim 16 wherein said nucleic acid is DNA.

19. The method of claim 18 wherein said DNA is gDNA.

20. The method of claim 16 wherein said nucleic acid is cDNA which is derived from said mRNA by reverse transcription of said mRNA.

21. The method of any of claims 16 to 20 wherein the nucleotide polymorphisms are located in the coding region of the *DGAT* gene.

22. The method of claim 21 wherein the nucleotide polymorphisms in the coding region of the gene encoding *DGAT* result in substitution, deletion and/or addition of at least one amino acid in the amino acid sequence of the polypeptide which is encoded by said gene.

23. The method of any of claims 16 to 22 wherein said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 1) a guanine and a cytosine residue which correlate with a predisposition for low fat content of milk and to low meat marbling.

24. The method of claim 23, wherein said nucleic acid molecule has at the position corresponding to position:
(a) 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine;
(b) 3343 a cytosine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine, and 11093 a thymine; or
(c) 3343 a guanine, 10433 a guanine, 10434 a cytosine, 11030 a guanine, 11048 a thymine and 11093 a thymine
which correlates with a predisposition for low fat content of milk and low meat marbling.

25. The method of claims 16 to 22 wherein said nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the *DGAT* gene (SEQ ID NO: 3) two adenine residues which correlate with a predisposition for high fat content of milk and high meat marbling.

26. The method of claim 25, wherein said nucleic acid molecule has at the position corresponding to position:
(a) 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 an adenosine, 11048 a cytosine and 11093 a thymine;
(b) 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 an adenosine, 11048 a cytosine and 11093 a cytosine;

(c) 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine and 11093 a thymine;
(d) 3343 a thymine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine and 11093 a cytosine;
(e) 3343 a cytosine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine, and 11093 a cytosine; or
(f) 3343 a thymine, 10433 an adenosine, 10434 an adenosine, 11030 a guanine, 11048 a cytosine, and 11093 a cytosine

which correlates with a predisposition for high fat content of milk and high meat marbling.

27. The method of any of claims 16 to 20 wherein the nucleotide polymorphisms are located in a region which is responsible for the regulation of the expression of the product of the gene encoding *DGAT*.

28. The method of any of claims 16 to 27 wherein the nucleotide polymorphisms are single nucleotide polymorphisms (SNP).

29. The method of any of claims 16 to 28, wherein said testing comprises hybridizing the nucleic acid molecule of claim 5 as a probe under stringent conditions to the nucleic acid molecules comprised in said sample and detecting hybridization.

30. The method of claim 29 further comprising digesting the product of said hybridization with a restriction endonuclease and analyzing the product of said digestion.

31. The method of claim 29, wherein said probe is detectably labeled.

32. The method of any of claims 16 to 28, wherein said testing comprises determining the nucleic acid sequence of at least a portion of said nucleic acid molecule.

33. The method of claim 32, wherein the determination of the nucleic acid sequence is effected by solid-phase minisequencing.

34. The method of any of claims 16 to 28 further comprising, prior to analyzing the nucleic acid, amplification of at least a portion of said nucleic acid.

35. The method of claim 34, wherein in the amplification reaction at least one of the primers employed in said amplification reaction is the primer of claim 8 or belongs to the primer pair of claim 8, comprising assaying for an amplification product.

36. The method of claim 34 or 35 wherein said amplification is effected by or said amplification is the polymerase chain reaction (PCR).

37. The method of any of claims 16 to 28 or 34 wherein the nucleic acid is analyzed by the use of:
(a) a primer extension assay;
(b) a differential hybridization assay; and/or
(c) an assay which detects allele-specific enzyme cleavage.

38. A method of testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling comprising:
(a) preparation of a tissue sample from the subject;
(b) contacting the sample with an antibody of claim 12 or 13; and
(c) detecting whether a specific binding of said antibody to its antigen has occurred.

39. The method of claim 36 wherein binding of the antibody of claim 12 indicates a predisposition of the mammal for low fat content of milk and to low meat marbling.

40. The method of claim 38 wherein binding of the antibody of claim 13 indicates a predisposition of the mammal for high fat content of milk and to high meat marbling.

41. The method of any of claims 16 to 40, wherein the sample is isolated from cloven hoofed animals.

42. The method of claim 41, wherein the cloven hoofed animals are cattle, buffalos, yaks or pigs.

43. A kit comprising at least the fragment of claim 4, the nucleic acid molecule of claim 5, the primer or primer pair of claim 8, or one of the antibodies of claim 12 or 13 in one or more container.

Figure 1

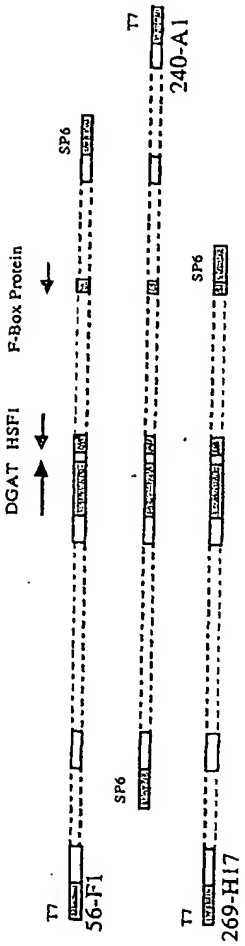

Figure 2

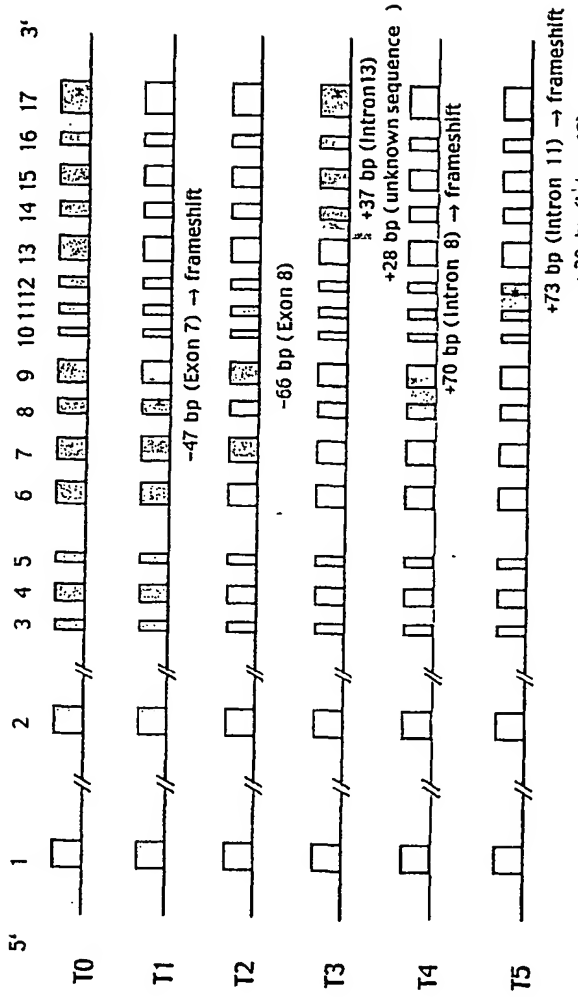
5'
1
2
3 4 5
6 7
8 9
10 11 12 13
14 15 16 17
3'
T0
T1
-47 bp (Exon 7) → frameshift
T2
-66 bp (Exon 8)
T3
+37 bp (Intron 13)
+28 bp (unknown sequence)
T4
+70 bp (Intron 8) → frameshift
T5
+73 bp (Intron 11) → frameshift
+ 20 bp (Intron 12)

Figure 3

1 CTGCCCCGAC AGGCCTGACA ACCAACAACA AGCCTTCCTC AATGCCACTA
51 GAGAAATGGG AAGTGCAGAC CCCTTCCTGC AGCCTGCTTT CCACATCCTG
101 ACTTCCAGAT TCAGGGGACA TGTCCCCACA CTGAGGAGGC TTTCCTTGGT
151 AGCTGGACCA GGCTGGTTGT GGGGAGGAGA TACCCAAGGA ATAAGAACCT
201 CCCATGGCCA CCCCCAGCCC TTAGGCTCTA GACAGGGTGA GTCAAGTTGA
251 GAAGATGAAT GGCAGGGCTG TGCTGGGCTC AGACAACCAA GGAACATAGA
301 CTCCTGCCCC AGCAAATGCC CTTGGTAACC AGCTAGGTAG GCATGAGCTA
351 AGAGGCTCCA AATCTTTGCA GACATGTGGT CAAACTGGAT CAGCCCAGGG
401 CCAGCACAGC TGTCTGCACC CTGGCAGGGG ACAGGCCCAC CAGACTCCAC
451 TGGTGTGGAC AGCAGGAAAG CCTGACCTGC AGTAGACCTG CTGCTTCAGG
501 GTGGGATCAC CTGAGGTGGG CACCCCCTTC TGGGGAGCAC TGTCAGCCTT
551 CATAACCTCA GGATGAAAGC CCCCAGTATT GGTAGAGCTT AGGTAGGCAT
601 CATTGCCCAA TCTGCATATG AAGAGTCTGA CCCTCAGGGA GAGAAGCAGC
651 TTGCCAAGGG CTGCCTTTGA CTTAAGCCCT GCTCCAGTTG GGCTTCCCTG
701 GTGGCTCAGA CCCTAAAGAA TCTGCCTGCA ATGTGGGAAA CCTGGGTTCA
751 GTCCCTGGGA CGGGAAGATC CCCTGGAGAA GGGATGGCAA CCCACTCCAG
801 TGTTCTTGCC TGAGAATCCC ACGGACAGAG GAGCCTGGCG GGCTGCAGTC
851 CATGGAGTCG CAAAGAGTCG GACACGACTG AGCAACTAAC ACTTTCACTT
901 TCTGCCCCAA TACCCCACCC ATCTGAACCT GAATACCTGA GTGGGTCCCA
951 CTGGCAGGAA GAGAGGCTCC TAGAGGCCCA GTCCTCCCCA AGGCTCCTCA
1001 GCTTTGGGGC CTGGATTGAC TGTTCCAGGA CTCTGATGGG CGGCTGGGGT
1051 GGATGACGGG TAGAGGCTGC CTCCCCAGTG ACTGGGACAG GCCTAGCCTT
1101 GTCTCCACAG GTGTCCATGG ACAGGACTTT GCAATCCAGA GGATGGGTGG
1151 TGTGGTGCAG GCTGCTGACC ACTGTGTCCA GGGTCTTCTC TCACGGGCCC
1201 AAGGCGCCTC CAACCTGGAG TCAGCCCAAG GCTCTTTCTA AATCCCCAAA
1251 CCCTTCCAGC CCTTCATTCC GCCAGCCTGC AGATTCCTCG TCCCAAGACA
1301 GATGTTGCTT CCACCAGGGG GAGATTCCTC ATTGAGCTTT CTTTCAACAA
1351 CTCCTCACGC ACATTTGTCC CCAAAAGACC CCACCTATCT TGACGTTTTC
1401 CCTCGTGCCT CTTCGCTGTG ACCCTGGCAG CACCTCAATC AGGATCCAGA
1451 GGTACCAGGG CTGT[illegible]
1501 [illegible]
1551 [illegible]AGGCCC CGCCCTGTAT CAACCTTGGA CCCCGTCTTC CTCAAACAGG
1601 CCCCGCCCCG CCTTGGTACA GAGGCCCTTC CTGATTGGTG CCTTCACAGT
1651 CCGTGCCTTC TCATTGGCTT GAGGCCCTGA TCTCTCAACT CCAGCGGTGG
1701 AACCCTTGGT TCCCTCACGT CCCGGGTCAG ATCGGTTCTC TTTGATGACC
1751 CTCGGCCCAC CCTGGTGTCC TCACTCCAGC TGTTTCATGT TAGCCGAAGG
1801 CAAAGGAGCC TGGACGCGGA CACAGGGAGC CGCCCCCAAC ACGTACCTTC
1851 ACTCGTCAGT GGCTACTGTG CTCAGCCTCT CCAGGCCAAC AGGCAGCCTG
1901 AGCCGTCAAT CTTCTCCTCT GCCAATCAGC GCGCCAGCCA GGCTGGCCCT
1951 CTAGTCAGGG CTCGGTACTG AAGGATGGCA AGTCCCGAAG GCTCCCAGGG
2001 ACGCGTGCGC ACGGGTTAGG GGGCTTCCCA CCAGCTGCCT GGGAGAGGGA
2051 TAGGGAGGGA AAGGCAGAGC TCCCGGGACT CAGCCCTGCT GCGCGTTCCT
2101 GAGAGGACTC TCTCCTCCTT CCATCCTCCC TTGGGAGCTA TACTGAGTCC
2151 TAGCGCTGAG TGGCCCAACT CTGCCTATGA ATAGACGAAG GTGCTTGGAC
2201 ACTGGCTAAG GGGATACTCC TGATCCACCG AGGCCGGGCC TGTGAGGAGG
2251 CAAGAGGGGT TCTCCAGCCT GATGAGGTCG CTCGAGCCCT TCCACACGCT
2301 ACTCCAAGAC ACGGGCCAGG TAGCTCCAGC CTGCCAGGTA AGGATGTCAG
2351 GCTGGCCTCA GCCGCAAATG GTCCAGTGGG AGAACATGTC ACCAGGGTCC
2401 CAGGTGCCTG TTGGTTGAGG TAAGAGGGTC AGGAGCGAGT CCGGCAGGAA

Figure 4

```
2451  GGAGGCTTGA TCTCAGGCTG AGCCTCTTGG TTTATTTGCT TTCAGAGAGG
2501  CGGTCTTCCC AGCTTTGCTT ACCCCATGGG AGTGAACGGA GTGGGTTCTG
2551  TGGCTAGGGG TGTTTCTTGT GTAAACCAGG CCTAAACTCC CGGTGAACCC
2601  TCGCATCTGG AGATCCAGGA TACTCACACT CCATGCTCTT TGCCAAATGT
2651  TTGTGAAACC AAGTAAGATC GGCCTTGCCC GCGCACGGGC CTCACTGTGC
2701  AGTTGTTTTG GTGTATTGGT TGCTTCATTC AACGACTGGA TGACTGCCGA
2751  CTGTGCAATG AAACAGAAAC CTCTGGGTCC CTGCGAATCA ACACCCCAGG
2801  ATCCTAACTC CCTGGCAAAA CTGGCCCAAG TGGGGAAGGC GGGAAGTTCT
2851  GCAAGTCTGC AGATGAAGGC AGAAGCGGGG CGGGTGGAGA GGCGGGCTGG
2901  CTTGTCTACT GTGGGGGCCT GGGCAGGGGA GAGGTGGCCA CCCTGGGAAT
2951  AGGTGGGCAT GGCACAAGTC CCGGAATGCG AGGACTGCGG CCTTTCTCCC
3001  CCTCCGTTCT CTGACCTGGC GCGTGTTTGA ACAGCCTAAG TGGAGGAAAA
3051  GTGGGTGCCT ACGGTGGTAA TTAGTGGGTT CACAGAGCAC GACCGTGCCG
3101  CGGGATGTAC GTTCGGTAGA CGCGTTGGGT GTCAGCCTGA CGTTAACGCA
3151  CTAGGCATTT CATAAATAAC TACAACCCCA AATTCTGCGC CTGAGCTGAG
3201  AAATGACGAA ATCCTGTGTT TATAGAGCGG GACAAGGGGC AGGCAGCGGT
3251  CAGCAGAGGC TTGTTTGCAG CTGCCCGGAA GCCCCGCGTG TTCCTCGTCT
3301  GTCCGGGATT GCATTTGCCA GGAGACCACA ACTCCCAGGG TG[illegible]ACCGCGC
3351  GCCAGCGGAC TACAAAGGTA TGCGCGCCGC GGCCCTGGGC CAGTTAGC[illegible]G
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3851  CAACCTGGTG GCCCAGGCCT GTCGGCGGCA GCTCGGGCTC GAGTCCGAGA
3901  GTCTGGCGCC TGGACCTTGG TGCACAGCTG TGCCCCTCGG GCCTCCACGG
3951  GGAAACTTAG CGGGAGGTTG GGGGCGGAGG GTCTCCTGCC CGGAACACCC
4001  AGGTACGGGG GCCGAGGGGA GGGCAGCGGC TCAACTTCTA GACGCCCTCC
4051  CTCTGCCTTC CTTTGGTGGG TTCTGAAGCT TTCCCAGGGT GAGCCCACTA
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4301  CGATTGACTG GCCTAGGATC CTGCTTATTA CCAGCACAAA TGGCTGCTCT
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4551  CCCCCTTTGC CATCCTCCAC GCCCCTCCCC CCAGCCCTGA CCTTCATCCT
4601  GGTCAAGGGC TCTCAGGGGC TCTGGTTTTG GGATCAGCTC CAGAGCTAGA
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4801  GCCGCAGCCC TGAAGAGTGA GAGCAAAGGT CAGGCACAGA GTTCAGGATG
4851  ACACCAGGGG AGGGTGGCTC TGTGAGGGGC ACTGGCTTCC TACAGGCCCC
4901  AGGTGGTCCT GAGGGGGCGG CTGCAAAGGC CAGGAGGCCC ACAGGCCCCT
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Figure 4 continued

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5351 CAGGCCCTTC CGGACATTTC CTGCTCACCT AGGTCTGGGC AGGCGGGGTC
5401 AGGTGCCGGG TGTGAGCTCA CTCCTTCCGG CAGCAAGGTG TAGCTATGTG
5451 CCGGAAGGAA GGCCGCTGCT GTTGCCTCGC CTCTGAGTGC ATCCCTTCCA
5501 GGTCCTCCAC ACTCCCCTGT GCCCCGACAC CTGGTGCGTC CTTCAGCCAT
5551 TGGTTCATGT GTCCTCCAGG CACAGCTTTC TAGTCCAGAG CCTCTAGGCT
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Figure 4 continued

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7651  CTACCGGGAG CATGCTCATG CCGTCCCTGC TGAATCCCAG GAGATGCCTG
7701  CAGAGGGCAG CCTGGGAGCC TCTGAGCTGG GGTCTGCGCC CCAGGGGGCA
7751  CTGGAGTCTC CCCAGGGGGC GAGAGAGAGT AGGCAGGGAT GGTCTGGTGG
7801  CCCTGGGTGG GGGATGGCTG CTCCGTGGGC CCAGGCCCTC CCTGGCAGCA
7851  CAGGTGAGTG GTCTTGGGGG TCCACGTAGA ACTTCCTCTT CTGTTCCAAA
7901  TTGCCCTCAT GGGTGCGGCA TGCCTGGGTG AACCTGGGGG AGCAGGGTGA
7951  GGACATGCTT CTCAGCCCAG CCCACAGCTC CAGGCCACAC TCTGCAGGAC
8001  TCTGGCCCCT CCCTCAGCCC TGGAGGGAGC AGGACTGGAG TCCTGTGTCC
8051  GCCTTGCTCT GACCTGGCCG AGGCCACTGC TGTGGGGCCC CAGCAGGCCT
8101  GCCCAGCAGA AGGTGGAGTG CAGGGACCCC AGGGGCAGCC TTCAGGGTGG
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8251  GCTCCAGAGG CTGCCTGTGT ACCAGGGGCC CCCACGCTTC TGTTTGTGGT
8301  TCTGGGCAGT CCCCTGGGGA GCGGTGGGGG CTGTGTGCCA GTCCAGACCC
8351  AGTAGTCCAC GCGTCCTGGT CTCTGGAGGC CGTGGCTGGT CCAGGACTGT
8401  GGCAAGGTGG TCGTGCAGGG CAGGCCCTCA GCAGCCTGTC TGTTCTCCTG
8451  CAGCCCCCAG CCTCCTGGCC CTTTGGTGCA CCCACAAAGC TCCCCCCTCC
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8601  GGACAGGCAA CTGCCAGTCG GCAGACATTG CAGGACCACG TGTGTCCTGG
8651  TAAGCTGGCT GGTTAGGTGT TTAGCTGGGG GATGGTGTGG CAGGTGGCCC
8701  CTGCATCTCT GAGCCTGTCA CCTCCTCGGG AAGCCTTCTG GGTGGGGGAC
8751  TCCACCCATG TCGCCTGGAG AAGCATCACT TTTCCACAGA GCCTTCTGCA
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8851  TGCAGAGGCC AGCCAGGCAT CTGGCCCCAG GCCACTGGCA AGAGCTCGTT
8901  GTGTTGGGGG ATCTGTCCTT TGCTGCTGCT GCAGGAGCGG CCGAGGCAGG
8951  CGGGGGCGTG AGTAGGGGTG GAGACCCAGG CCCAGCTTCC CCAGCCCCTC
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9751  [redacted]GTAAGC
9801  AGTGCCCTCA CGCCCTCCCC TGACTTGCCT CAAGGTCCTT ACCAGTCGGG
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Figure 4 continued

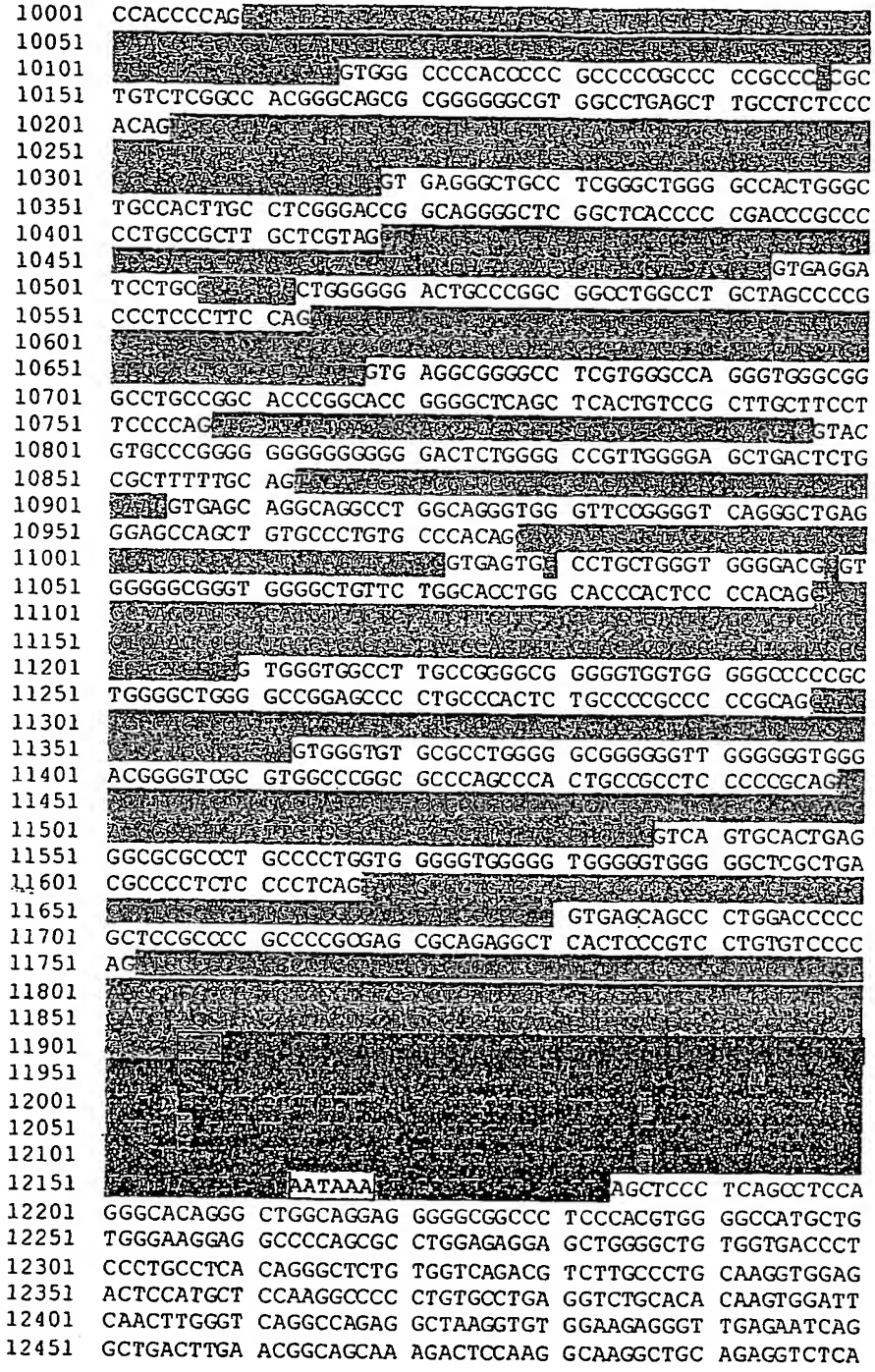

Figure 4 continued

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12351  ACTCCATGCT CCAAGGCCCC CTGTGCCTGA GGTCTGCACA CAAGTGGATT
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12601  CCCTTGGGGG CAGAGGTTGG CCTGATGCCA GGGGCTCCCC GTTTTTCCAG
12651  GCCCTCAGCA GGTAGTTGGG TGTGGCCCTC AGGATACCTT GGTCCCAGAG
12701  CTTGCCACTC AAAAAGCTTG GCAGTGAGGC AAGGGCAACC CCGGGCTGTT
12751  CCCCCCTCTA CTGGCTCTGC CGCCTGGGTT GGAAACCCTG AGGCTGTGCC
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12901  AAGCCGCTCT AGCCCATGGT GGTCGTCTGG GCGAGACAGG CTGGTTGGCT
12951  AGGCACTGTT TGGTCTACAG CAGGTGTAGG CAGCGTCTCC CTGACCCCTG
13001  CCTCCTAGGA AGCCACCACC CTGGGCCCTA CTCATCAGCA AGGACAGCGA
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13101  ACATGCACCT CTGCACCCCC TGCTGCCTGA CTCAGGAGTG GGGGGGGGGG
13151  TCCTGTGCTT CCTTCACTCC AGACCCACGG TGCTGACCCA GTGCACCCAC
13201  CTGGTCCTCT AGTGCGGACC TGGCCACAGG GCTCCTGTGG GCCCACGCTG
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13351  TTCCGAGACA CTGCGCATCA TGCCCCCCTC CACCCCCACC CACACTGGCA
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13501  [redacted]ATGAA
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SINE Sequence
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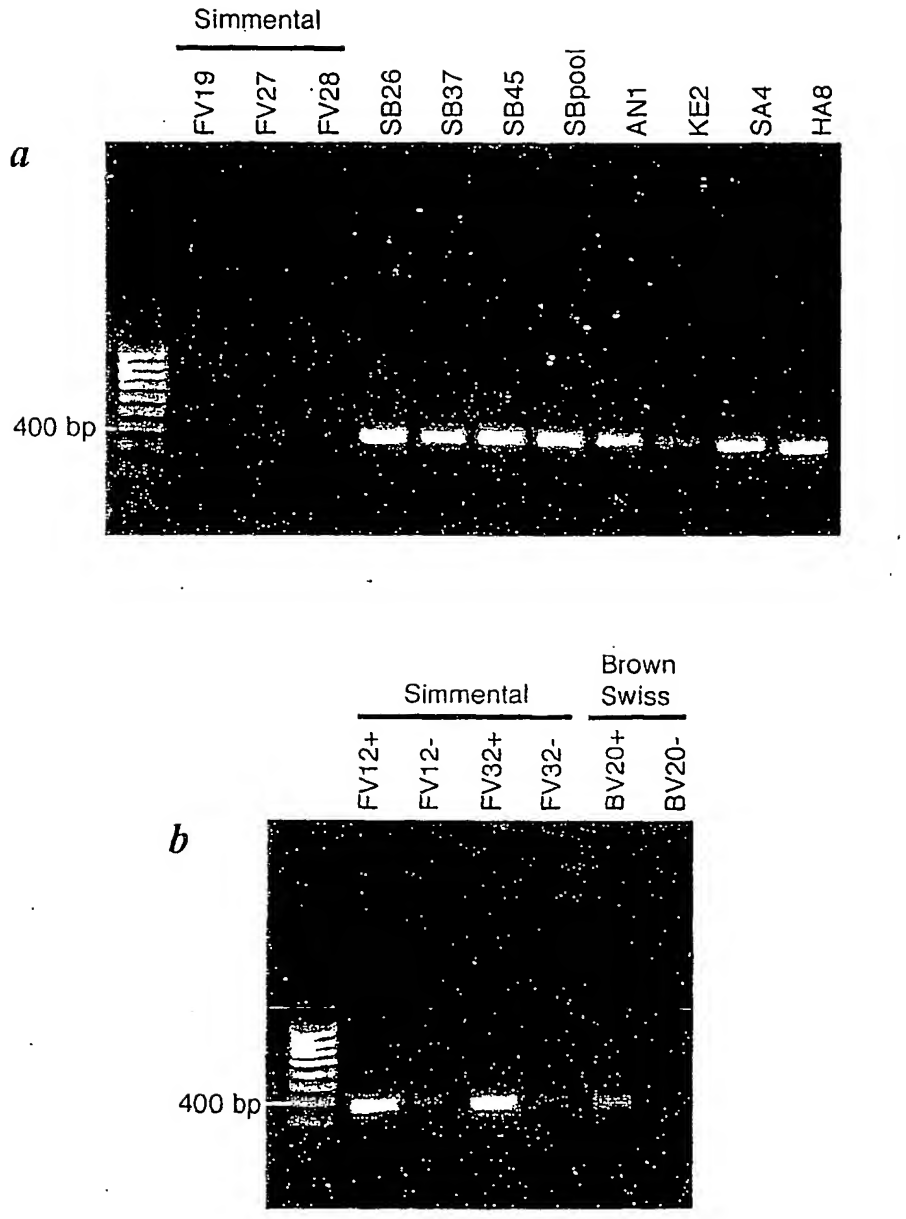
Figure 4 continued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FV19
FV27
FV28
SB26
SB37
SB45
SBpool
AN1
KE2
SA4
HA8
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Simmental
Brown Swiss
FV12+
FV12-
FV32+
FV32-
BV20+
BV20-
b
400 bp

Figure 5

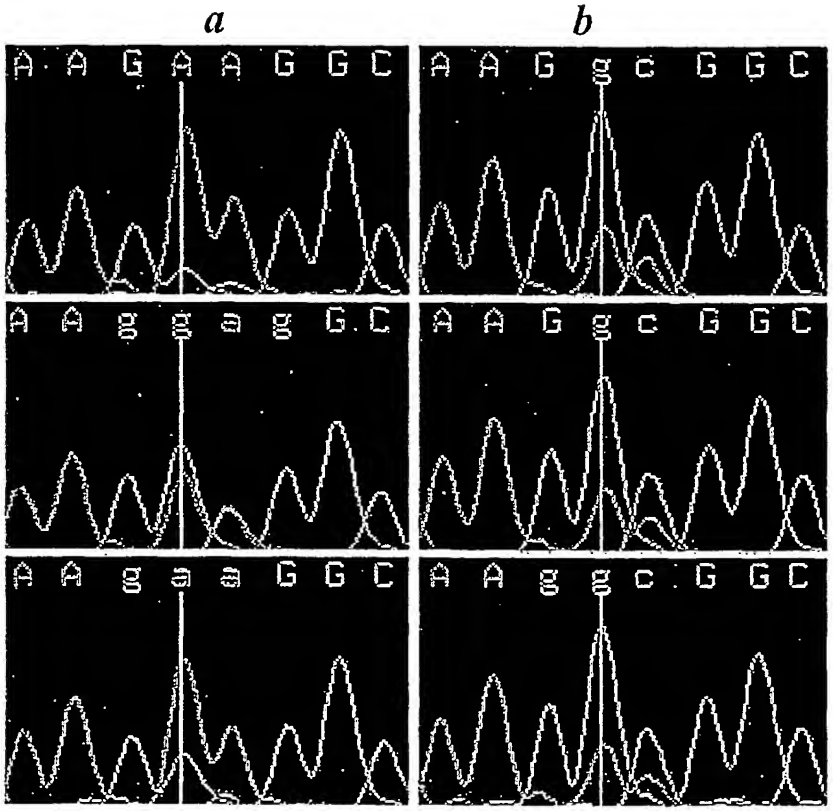
a
b
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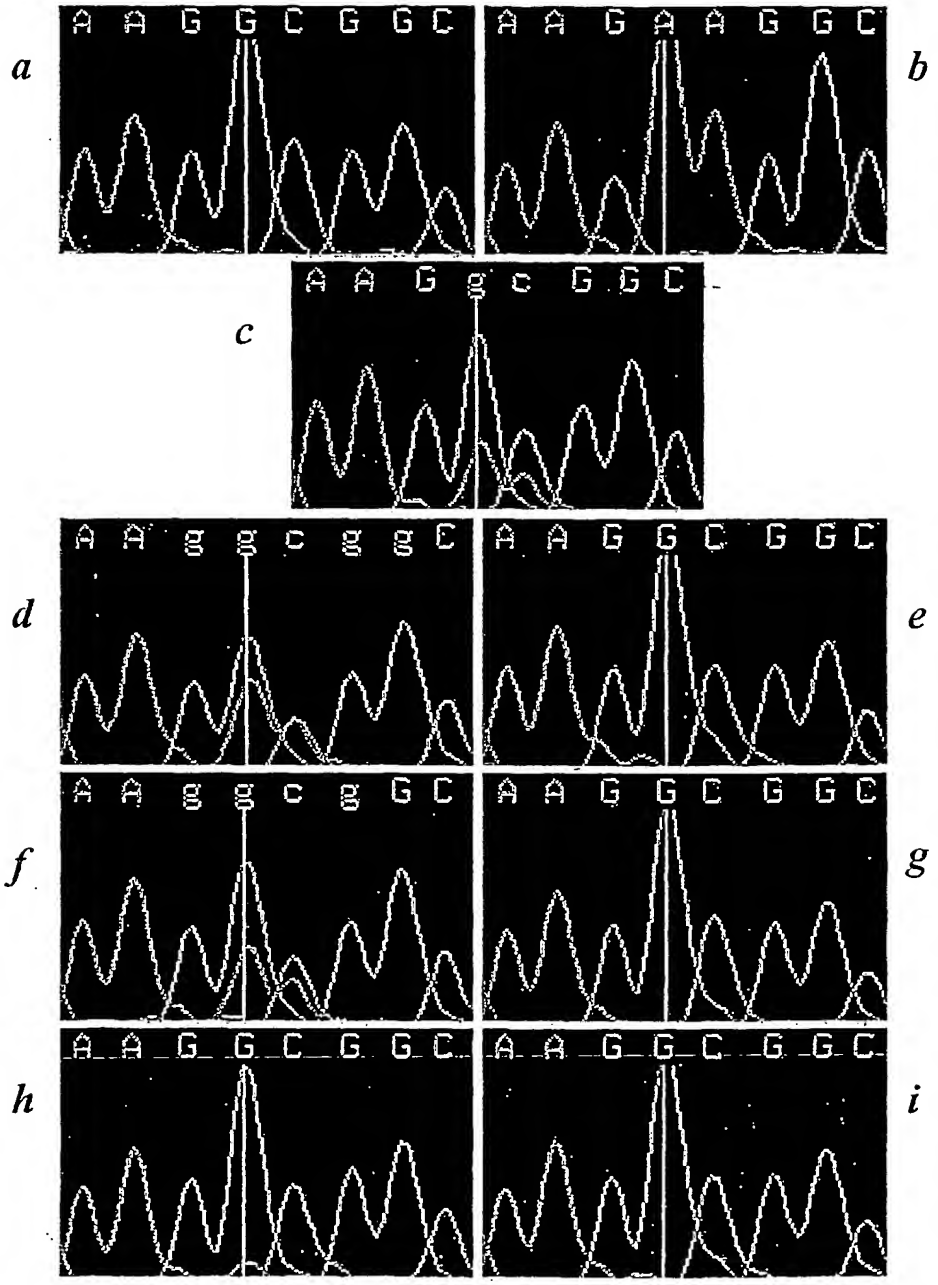
Figure 6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b
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c
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h
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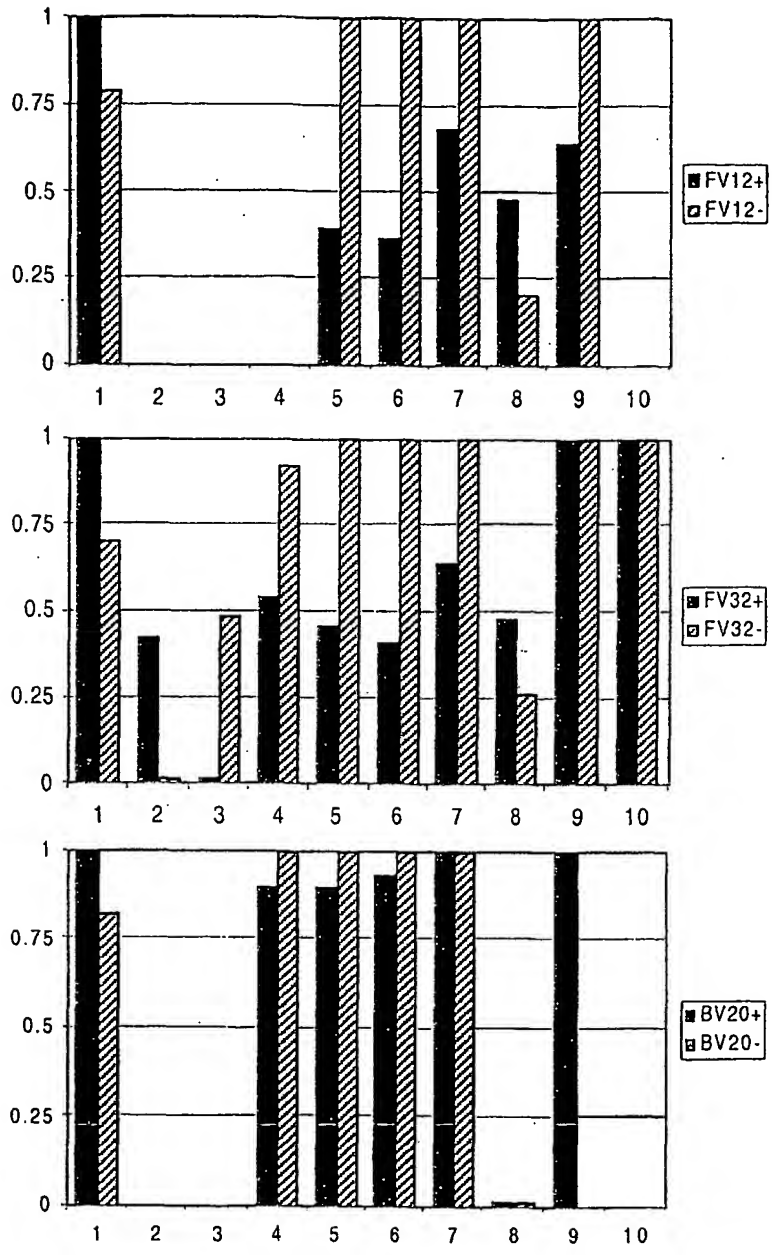
i
A A G G C G G C

Figure 7



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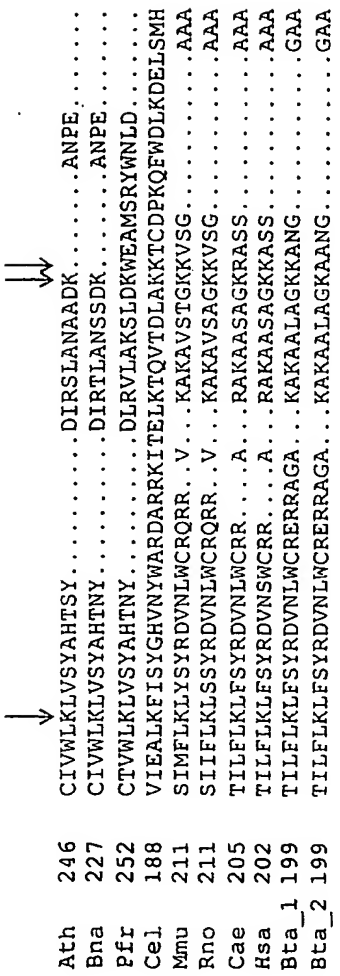
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Cel 188 VIEALKFISYGHVNYWARDARRKITELKTQVTDLAKKTCDPKQFWDLKDELSMH
Mmu 211 SIMFLKLYSYRDVNLWCRQRR..V...KAKAVSTGKKVSG.....AAA
Rno 211 SIIFLKLSSYRDVNLWCRQRR..V...KAKAVSAGKKVSG.....AAA
Cae 205 TILFLKLFSYRDVNLWCRR.....A...RAKAASAGKRASS.....AAA
Hsa 202 TILFLKLFSYRDVNSWCRR.....A...RAKAASAGKKASS.....AAA
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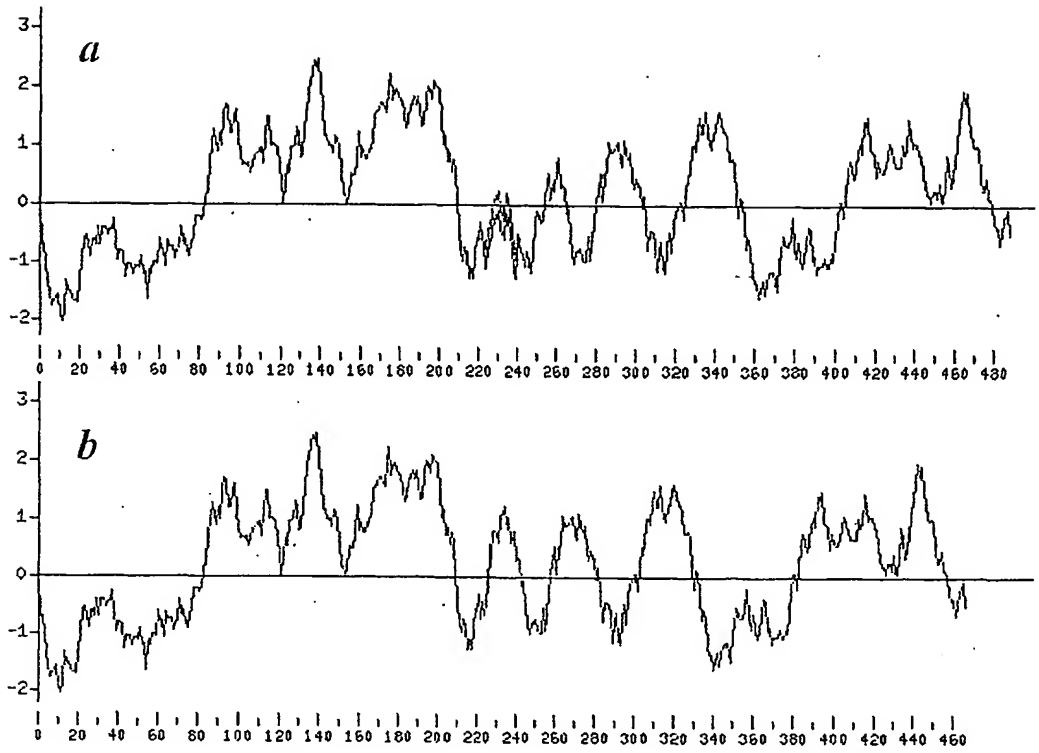
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b
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2
1
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-1
-2
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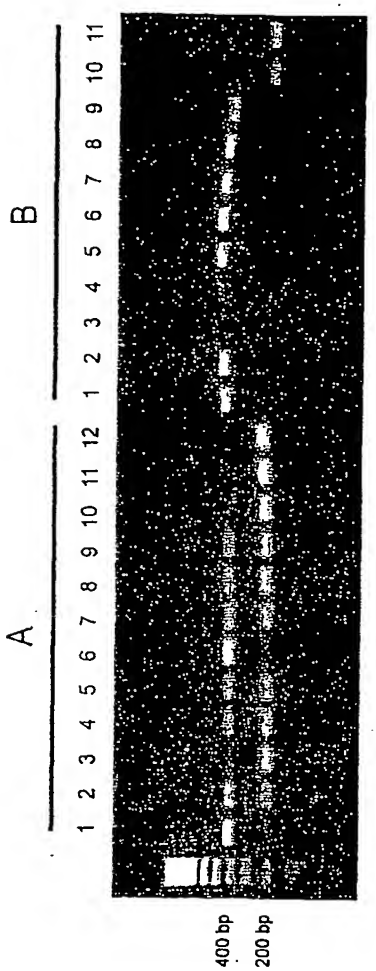

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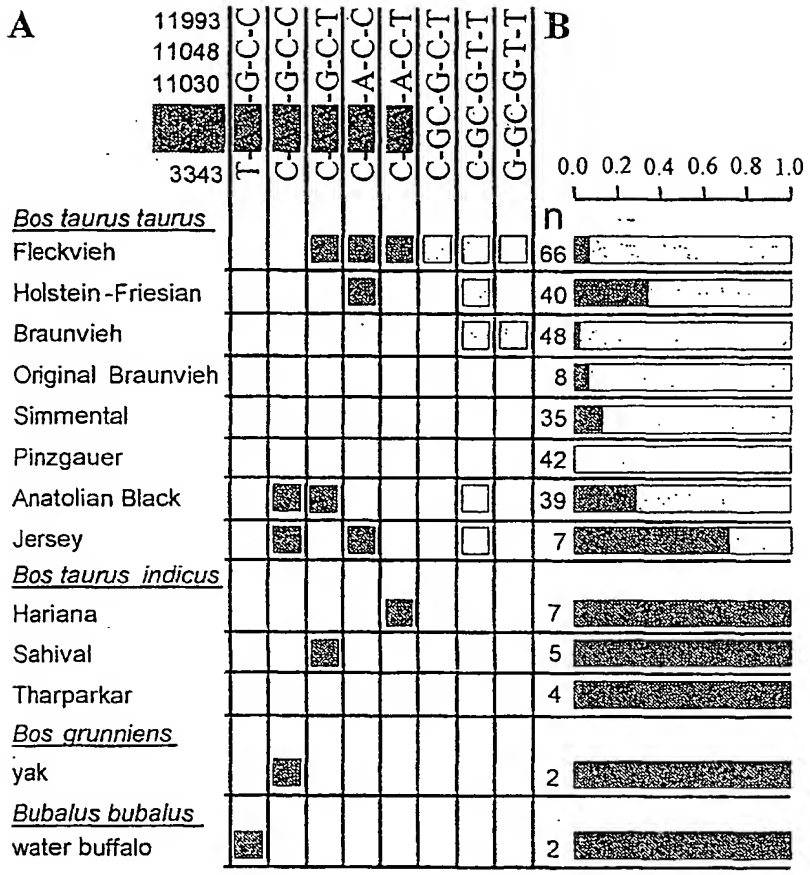
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C-GC-G-C-T
C-GC-G-T-T
G-GC-G-T-T
B
0.0 0.2 0.4 0.6 0.8 1.0
n
Bos taurus taurus
Fleckvieh 66
Holstein-Friesian 40
Braunvieh 48
Original Braunvieh 8
Simmental 35
Pinzgauer 42
Anatolian Black 39
Jersey 7
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Sahival 5
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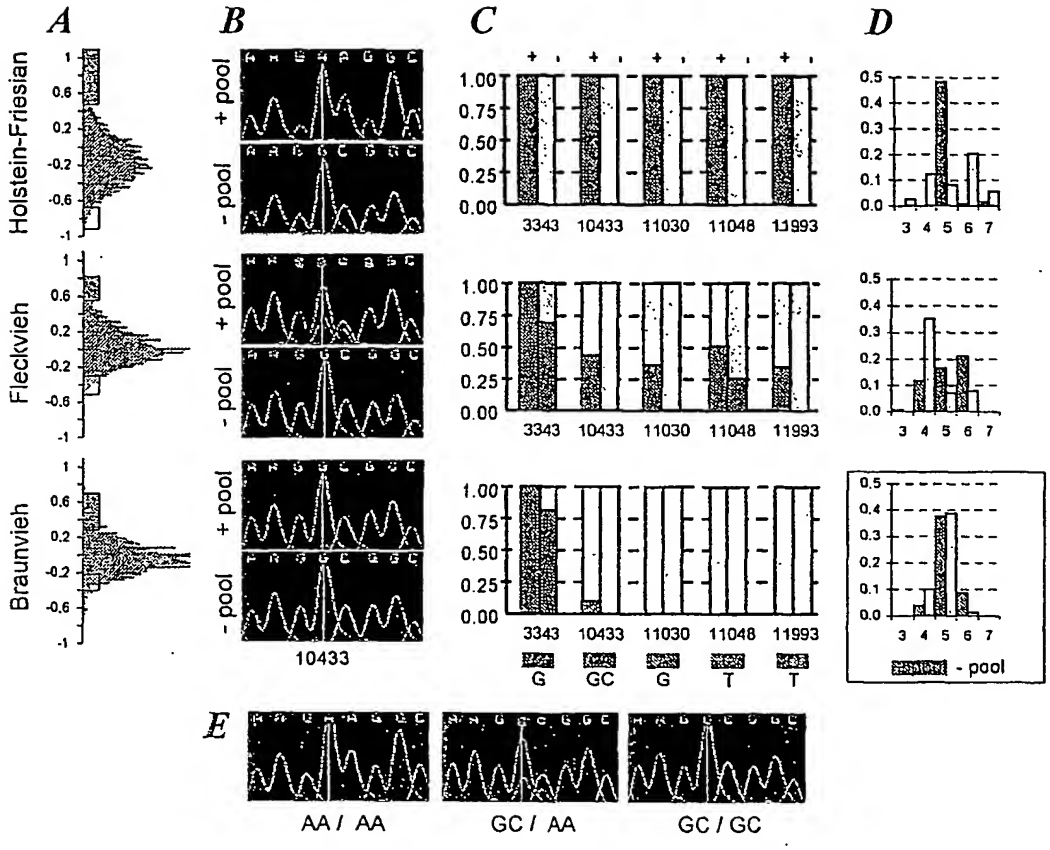
Bos grunniens
yak 2
Bubalus bubalus
water buffalo 2

Figure 12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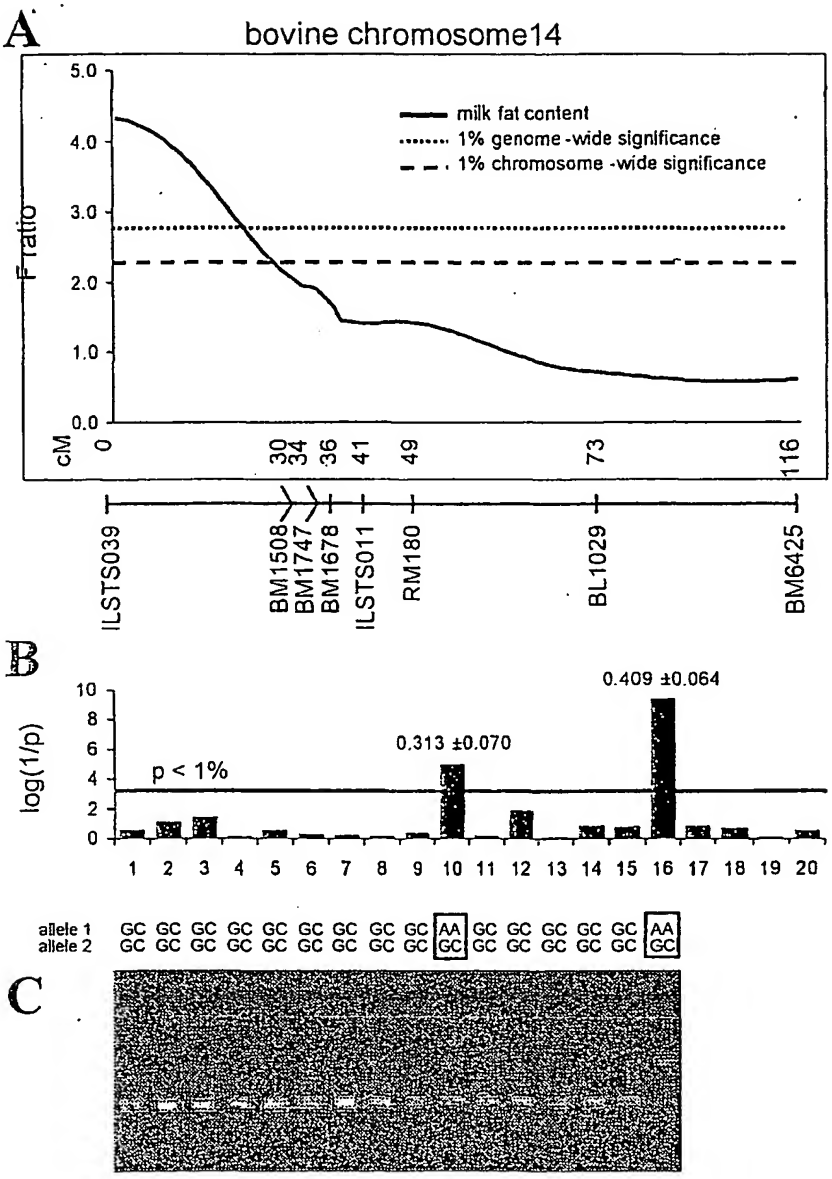
B
C
D
Holstein-Friesian
Fleckvieh
Braunvieh
+ pool
- pool
10433
3343 10433 11030 11048 11993
G GC G T T
- pool
E
AA / AA
GC / AA
GC / GC

Figure 13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1% genome -wide significance
1% chromosome -wide significance
F ratio
cM
ILSTS039
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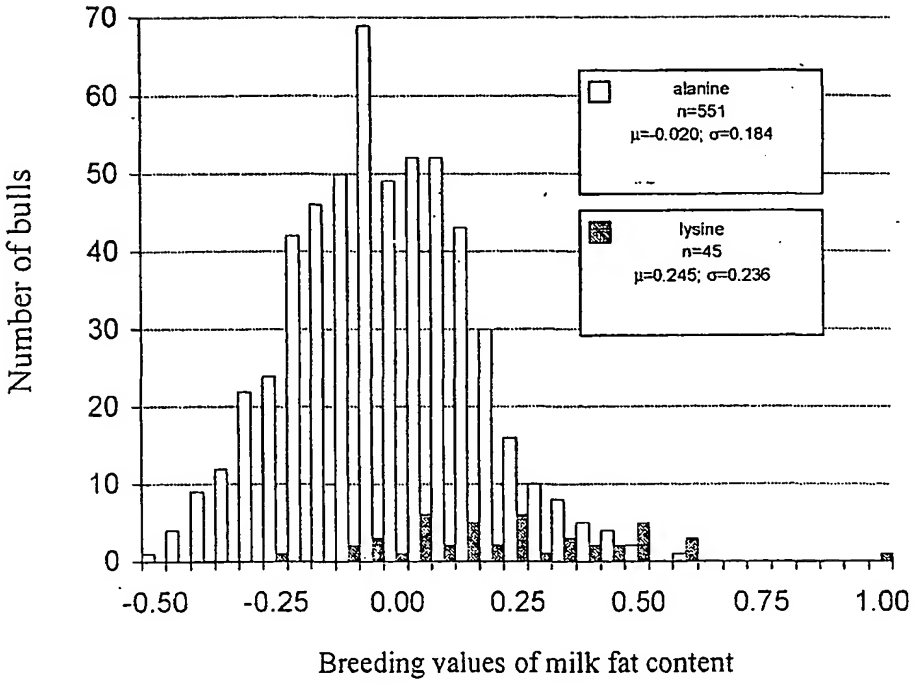
BM1747
BM1678
ILSTS011
RM180
BL1029
BM6425
B
log(1/p)
p < 1%
0.313 ±0.070
0.409 ±0.064
allele 1
allele 2
C

Figure 14

Bull 899: 5-C-AA-A-C-C (HF)
6-G-GC-G-T-T

Bull 705: 6-C-AA-G-C-T (FV)
4-C-GC-G-T-T

Figure 15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50
40
30
20
10
0
Number of bulls
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μ=-0.020; σ=0.184
lysine
n=45
μ=0.245; σ=0.236
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-0.25
0.00
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1.00
Breeding values of milk fat content

Figure 16

SEQUENCE LISTING

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         35                  40                  45

Asp Lys Asp Gly Asp Val Asp Val Gly Ser Gly His Trp Asn Leu Arg
     50                  55                  60

Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser
 65                  70                  75                  80

Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser
                 85                  90                  95

Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val
            100                 105                 110

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
        115                 120                 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
    130                 135                 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
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Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
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Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
            180                 185                 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
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Leu Phe Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro
            260                 265                 270

Arg Ile Arg Lys Arg Phe Leu Leu Arg Arg Leu Leu Glu Met Leu Phe
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Gly Gln Pro Val Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu
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